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PATENT APPLICATION

INDUCING CELLULAR IMMUNE RESPONSES TO PROSTATE CANCER ANTIGENS USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to provisional application 60/171,312 filed 12/21/99. This application is related to U.S.S.N. 09/189,702, filed 11/10/98, which is a CIP of U.S.S.N 08/205,713 filed 3/4/94, which is a CIP of abandoned U.S.S.N. 08/159,184 filed 11/29/93, which is a CIP of abandoned U.S.S.N. 08/073,205 filed 6/4/93 which is a CIP of abandoned U.S.S.N 08/027,146 filed 3/5/93. The present application is also related to U.S.S.N. 09/226,775, which is a CIP of abandoned U.S.S.N. 08/815,396, which claims benefit of abandoned U.S.S.N. 60/013,113. Furthermore, the present application is related to U.S.S.N. 09/017,735, which is a CIP of abandoned U.S.S.N. 08/589,108; U.S.S.N. 08/454,033; and U.S.S.N. 08/349,177. The present application is also related to U.S.S.N. 09/017,524, U.S.S.N. 08/821,739, which claims benefit of abandoned U.S.S.N. 60/013,833; and U.S.S.N. 08/347,610, which is a CIP of U.S.S.N. 08/159,339, which is a CIP of abandoned U.S.S.N. 08/103,396, which is a CIP of abandoned U.S.S.N. 08/027,746, which is a CIP of abandoned U.S.S.N. 07/926,666. The present application is also related to U.S.S.N. 09/017,743, which is a CIP of abandoned U.S.S.N. 08/590,298; and U.S.S.N. 08/452,843, which is a CIP of U.S.S.N. 08/344,824, which is a CIP of abandoned U.S.S.N. 08/278,634. The present application is also related to PCT application 99/12066 filed 5/28/99 which claims benefit of provisional U.S.S.N. 60/087,192, and U.S.S.N. 09/009,953, which is a CIP of abandoned U.S.S.N. 60/036,713 and abandoned U.S.S.N. 60/037,432. In addition, the present application is related to U.S.S.N. 09/098,584, U.S.S.N. 09/239,043, U.S.S.N. 60/117,486, U.S.S.N. 09/350,401, and U.S.S.N. 09/357,737. In addition, the present application is related to U.S. Patent Application entitled "Inducing Cellular Immune Responses to Carcinoembryonic Antigen Using Peptide and Nucleic Acid Compositions", Attorney Docket No. 018623-014400, filed 12/10/99; U.S. Patent Application entitled "Inducing Cellular Immune Responses to p53 Using Peptide and Nucleic Acid Compositions"; Attorney Docket No. 018623-014500, filed 12/10/99; U.S. Patent Application entitled "Inducing Cellular Immune Responses to MAGE2/3 Using Peptide and Nucleic Acid Compositions", Attorney Docket No. 018623-014600, filed 12/10/99; and U.S. Patent

Application entitled "Inducing Cellular Immune Responses to HER2/neu Using Peptide and Nucleic Acid Compositions", Attorney Docket No. 018623-014800, filed 12/10/99. All of the above applications are incorporated herein by reference.

FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

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I. BACKGROUND OF THE INVENTION

A growing body of evidence suggests that cytotoxic T lymphocytes (CTL) are important in the immune response to tumor cells. CTL recognize peptide epitopes in the context of HLA class I molecules that are expressed on the surface of almost all nucleated cells. Following intracellular processing of endogenously synthesized tumor antigens, antigen-derived peptide epitopes bind to class I HLA molecules in the endoplasmic reticulum, and the resulting complex is then transported to the cell surface. CTL recognize the peptide-HLA class I complex, which then results in the destruction of the cell bearing the HLA-peptide complex directly by the CTL and/or via the activation of non-destructive mechanisms, *e.g.*, activation of lymphokines such as tumor necrosis factor-α (TNF- α) or interferon-γ (IFNγ) which enhance the immune response and facilitate the destruction of the tumor cell.

Tumor-specific helper T lymphocytes (HTLs) are also known to be important for maintaining effective antitumor immunity. Their role in antitumor immunity has been demonstrated in animal models in which these cells not only serve to provide help for induction of CTL and antibody responses, but also provide effector functions, which are mediated by direct cell contact and also by secretion of lymphokines (*e.g.*, IFNγ and TNF- α).

A fundamental challenge in the development of an efficacious tumor vaccine is immune suppression or tolerance that can occur. There is therefore a need to establish vaccine embodiments that elicit immune responses of sufficient breadth and vigor to prevent progression and/or clear the tumor.

The epitope approach, as we have described, represents a solution to this challenge, in that it allows the incorporation of various CTL, HTL, and antibody (if desired) epitopes from discrete regions of one or more target tumor-associated antigens (TAAs) in a single vaccine composition. Such a composition may simultaneously target multiple dominant and subdominant epitopes and thereby be used to achieve effective immunization in a diverse population.

Prostate cancer is the most common malignancy in men. Current therapies, *i.e.*, chemotherapy combined with androgen blockade, antiandrogen withdrawal, and other secondary hormonal therapies, have met with limited success. Thus, there is a need to develop more efficacious therapies. The multiepitopic immunotherapy vaccine compositions of the present invention fulfill this need.

Antigens that are associated with prostate cancer include, but are not limited to, prostate specific antigen (PSA), prostate specific membrane antigen (PSM), prostatic acid phosphatase (PAP), and human kallikrein2 (hK2 or HuK2). These antigens represent important antigen targets for the polyepitopic vaccine compositions of the invention.

PSM is also an important candidate for prostate cancer therapy. It is a Type II membrane protein that is expressed at high levels on prostate adenocarcinomas. The levels of expression increase on metastases and in carcinomas that are refractory to hormone therapy. PSM is not generally present on normal tissues, although low levels have been detected in the colonic crypts and in the duodenum, and PSM can be detected in normal male serum and seminal fluid (*see, e.g.*, Silver *et al.*, *Clin. Cancer Res.* 3:81-85, 1997). CTL responses to PSM have also been documented (*see, e.g.*, Murphy *et al.*, *Prostate* 29:371-380, 1996; and Salgaller *et al.*, *Prostate* 35:144-151, 1998).

PAP is a tissue-specific differentiation antigen that is secreted exclusively by cells in the prostate (*see, e.g.*, Lam *et al.*, *Prostate* 15:13-21, 1989). It can be detected in serum and levels are increased in patients with prostate carcinoma (*see, e.g.*, Jacobs *et al.*, *Curr. Probl. Cancer* 15:299-360, 1991). The PAP protein sequence has, at best, a 49% sequence homology with other acid phosphatases with the homologous regions distributed throughout the protein. Accordingly, PAP-specific epitopes can be identified and several different CTL epitopes have been described (*see, e.g.*, Peshwa *et al.*, *Prostate* 36:129-138, 1998).

The hK2 protein is functionally a serine protease involved in posttranslational processing of polypeptides. It is expressed by prostate epithelia exclusively, and is found in both benign and malignant prostate cancer tissue. Although it is expressed in 50% of normal prostate cells, the percentage of cells expressing hK2 is increased in adenocarcinomas and prostatic intraepithelial neoplasia (PIN) (*see, e.g.*, Darson *et al.*, *Urology* 49:857-862, 1997). Based on the preferential expression of this antigen on prostate cancer cells, hK2 is also an important target for immunotherapy.

Prostate-specific antigen (PSA), also referred to as hK3, is a secreted serine protease and a member of the kallikrein family of proteins. The PSA gene is 80% homologous with the hK2 gene, however, tissue expression of hK2 is regulated independently of PSA (*see, e.g.*, Darson *et al.*, *Urology* 49:857-862, 1997). Expression of PSA is restricted to prostate epithelial cells, both benign and malignant. The antigen can be detected in the serum of most prostate cancer patients and in seminal plasma. Several

T cell epitopes from PSA have been identified and have been found to be immunogenic, and antibody responses have been reported in patients (*see, e.g.*, Correale *et al.*, *J. Immunol.* 161:3186, 1998; and Alexander *et al.*, *Urology* 51:150-157, 1998). Thus, based on its prostate-restricted expression and ability to stimulate immune responses, PSA is an attractive target for immunotherapy of prostate cancer.

The information provided in this section is intended to disclose the presently understood state of the art as of the filing date of the present application. Information is included in this section which was generated subsequent to the priority date of this application. Accordingly, information in this section is not intended, in any way, to delineate the priority date for the invention.

II. SUMMARY OF THE INVENTION

This invention applies our knowledge of the mechanisms by which antigen is recognized by T cells, for example, to develop epitope-based vaccines directed towards TAAs. More specifically, this application identifies epitopes for inclusion in diagnostic and/or pharmaceutical compositions and methods of use of the epitopes for the evaluation of immune responses and for the treatment and/or prevention of cancer.

The use of epitope-based vaccines has several advantages over current vaccines, particularly when compared to the use of whole antigens in vaccine compositions. For example, immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-based vaccines. Such immunosuppressive epitopes may, *e.g.*, correspond to immunodominant epitopes in whole antigens, which may be avoided by selecting peptide epitopes from non-dominant regions (*see, e.g.*, Disis *et al.*, *J. Immunol.* 156:3151-3158, 1996).

An additional advantage of an epitope-based vaccine approach is the ability to combine selected epitopes (CTL and HTL), and further, to modify the composition of the epitopes, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches.

Another major benefit of epitope-based immune-stimulating vaccines is their safety. The possible pathological side effects caused by infectious agents or whole protein antigens, which might have their own intrinsic biological activity, is eliminated.

An epitope-based vaccine also provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen (a "pathogen"

may be an infectious agent or a tumor-associated molecule). Thus, patient-by-patient variability in the immune response to a particular pathogen may be alleviated by inclusion of epitopes from multiple antigens from the pathogen in a vaccine composition.

Furthermore, an epitope-based anti-tumor vaccine also provides the opportunity to combine epitopes derived from multiple tumor-associated molecules. This capability can therefore address the problem of tumor-to tumor variability that arises when developing a broadly targeted anti-tumor vaccine for a given tumor type and can also reduce the likelihood of tumor escape due to antigen loss. For example, prostate cancer cells in one patient may express target TAAs that differ from the prostate cancer cells in another patient. Epitopes derived from multiple TAAs can be included in a polyepitopic vaccine that will target both prostate cancers.

One of the most formidable obstacles to the development of broadly efficacious epitope-based immunotherapeutics, however, has been the extreme polymorphism of HLA molecules. To date, effective non-genetically biased coverage of a population has been a task of considerable complexity; such coverage has required that epitopes be used that are specific for HLA molecules corresponding to each individual HLA allele. Impractically large numbers of epitopes would therefore have to be used in order to cover ethnically diverse populations. Thus, there has existed a need for peptide epitopes that are bound by multiple HLA antigen molecules for use in epitope-based vaccines. The greater the number of HLA antigen molecules bound, the greater the breadth of population coverage by the vaccine.

Furthermore, as described herein in greater detail, a need has existed to modulate peptide binding properties, *e.g.*, so that peptides that are able to bind to multiple HLA molecules do so with an affinity that will stimulate an immune response. Identification of epitopes restricted by more than one HLA allele at an affinity that correlates with immunogenicity is important to provide thorough population coverage, and to allow the elicitation of responses of sufficient vigor to prevent or clear an infection in a diverse segment of the population. Such a response can also target a broad array of epitopes. The technology disclosed herein provides for such favored immune responses.

In a preferred embodiment, epitopes for inclusion in vaccine compositions of the invention are selected by a process whereby protein sequences of known antigens are evaluated for the presence of motif or supermotif-bearing epitopes. Peptides corresponding to a motif- or supermotif-bearing epitope are then synthesized and tested for the ability to bind to the HLA molecule that recognizes the selected motif. Those

peptides that bind at an intermediate or high affinity *i.e.*, an IC_{50} (or a K_D value) of about 500 nM or less for HLA class I molecules or an IC_{50} of about 1000 nM or less for HLA class II molecules, are further evaluated for their ability to induce a CTL or HTL response. Immunogenic peptide epitopes are selected for inclusion in vaccine compositions.

Supermotif-bearing peptides may additionally be tested for the ability to bind to multiple alleles within the HLA supertype family. Moreover, peptide epitopes may be analoged to modify binding affinity and/or the ability to bind to multiple alleles within an HLA supertype.

The invention also includes embodiments comprising methods for monitoring or evaluating an immune response to a TAA in a patient having a known HLA-type. Such methods comprise incubating a T lymphocyte sample from the patient with a peptide composition comprising a TAA epitope that has an amino acid sequence comprising a supermotif or motif and which binds the product of at least one HLA allele present in the patient, and detecting for the presence of a T lymphocyte that binds to the peptide. A CTL peptide epitope may, for example, be used as a component of a tetrameric complex for this type of analysis.

An alternative modality for defining the peptide epitopes in accordance with the invention is to recite the physical properties, such as length; primary structure; or charge, which are correlated with binding to a particular allele-specific HLA molecule or group of allele-specific HLA molecules. A further modality for defining peptide epitopes is to recite the physical properties of an HLA binding pocket, or properties shared by several allele-specific HLA binding pockets (*e.g.* pocket configuration and charge distribution) and reciting that the peptide epitope fits and binds to the pocket or pockets.

As will be apparent from the discussion below, other methods and embodiments are also contemplated. Further, novel synthetic peptides produced by any of the methods described herein are also part of the invention.

III. BRIEF DESCRIPTION OF THE FIGURES

not applicable

IV. DETAILED DESCRIPTION OF THE INVENTION

The peptide epitopes and corresponding nucleic acid compositions of the present invention are useful for stimulating an immune response to a TAA by stimulating

the production of CTL or HTL responses. The peptide epitopes, which are derived directly or indirectly from native TAA protein amino acid sequences, are able to bind to HLA molecules and stimulate an immune response to the TAA. The complete sequence of the TAA proteins to be analyzed can be obtained from GenBank. Peptide epitopes and analogs thereof can also be readily determined from sequence information that may subsequently be discovered for heretofore unknown variants of particular TAAs, as will be clear from the disclosure provided below.

A list of target TAAs includes, but is not limited to, the following antigens: MAGE 1, MAGE 2, MAGE 3, MAGE-11, MAGE-A10, BAGE, GAGE, RAGE, MAGE-C1, LAGE-1, CAG-3, DAM, MUC1, MUC2, MUC18, NY-ESO-1, MUM-1, CDK4, BRCA2, NY-LU-1, NY-LU-7, NY-LU-12, CASP8, RAS, KIAA-2-5, SCCs, p53, p73, CEA, Her 2/neu, Melan-A, gp100, tyrosinase, TRP2, gp75/TRP1, kallikrein, PSM, PAP, PSA, PT1-1, B-catenin, PRAME, Telomerase, FAK, cyclin D1 protein, NOEY2, EGF-R, SART-1, CAPB, HPVE7, p15, Folate receptor CDC27, PAGE-1, and PAGE-4. Epitopes derived from these antigens may be used in combination with one another to target a specific tumor type, *e.g.*, prostate tumors, or to target multiple types of tumors.

The peptide epitopes of the invention have been identified in a number of ways, as will be discussed below. Also discussed in greater detail is that analog peptides have been derived and the binding activity for HLA molecules modulated by modifying specific amino acid residues to create peptide analogs exhibiting altered immunogenicity. Further, the present invention provides compositions and combinations of compositions that enable epitope-based vaccines that are capable of interacting with HLA molecules encoded by various genetic alleles to provide broader population coverage than prior vaccines.

IV.A. Definitions

The invention can be better understood with reference to the following definitions, which are listed alphabetically:

A "construct" as used herein generally denotes a composition that does not occur in nature. A construct can be produced by synthetic technologies, *e.g.*, recombinant DNA preparation and expression or chemical synthetic techniques for nucleic or amino acids. A construct can also be produced by the addition or affiliation of one material with another such that the result is not found in nature in that form.

A "computer" or "computer system" generally includes: a processor; at least one information storage/retrieval apparatus such as, for example, a hard drive, a disk drive or a tape drive; at least one input apparatus such as, for example, a keyboard, a mouse, a touch screen, or a microphone; and display structure. Additionally, the computer may include a communication channel in communication with a network. Such a computer may include more or less than what is listed above.

"Cross-reactive binding" indicates that a peptide is bound by more than one HLA molecule; a synonym is degenerate binding.

A "cryptic epitope" elicits a response by immunization with an isolated peptide, but the response is not cross-reactive *in vitro* when intact whole protein which comprises the epitope is used as an antigen.

A "dominant epitope" is an epitope that induces an immune response upon immunization with a whole native antigen (see, *e.g.*, Sercarz, *et al.*, *Annu. Rev. Immunol.* 11:729-766, 1993). Such a response is cross-reactive *in vitro* with an isolated peptide epitope.

With regard to a particular amino acid sequence, an "epitope" is a set of amino acid residues which is involved in recognition by a particular immunoglobulin, or in the context of T cells, those residues necessary for recognition by T cell receptor proteins and/or Major Histocompatibility Complex (MHC) receptors. In an immune system setting, *in vivo* or *in vitro*, an epitope is the collective features of a molecule, such as primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Throughout this disclosure epitope and peptide are often used interchangeably.

It is to be appreciated that protein or peptide molecules that comprise an epitope of the invention as well as additional amino acid(s) are within the bounds of the invention. In certain embodiments, there is a limitation on the length of a peptide of the invention which is not otherwise a construct as defined herein. An embodiment that is length-limited occurs when the protein/peptide comprising an epitope of the invention comprises a region (i.e., a contiguous series of amino acids) having 100% identity with a native sequence. In order to avoid a recited definition of epitope from reading, *e.g.*, on whole natural molecules, the length of any region that has 100% identity with a native peptide sequence is limited. Thus, for a peptide comprising an epitope of the invention and a region with 100% identity with a native peptide sequence (and which is not otherwise a construct), the region with 100% identity to a native sequence generally has a

length of: less than or equal to 600 amino acids, often less than or equal to 500 amino acids, often less than or equal to 400 amino acids, often less than or equal to 250 amino acids, often less than or equal to 100 amino acids, often less than or equal to 85 amino acids, often less than or equal to 75 amino acids, often less than or equal to 65 amino acids, and often less than or equal to 50 amino acids. In certain embodiments, an "epitope" of the invention which is not a construct is comprised by a peptide having a region with less than 51 amino acids that has 100% identity to a native peptide sequence, in any increment of (50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5) down to 5 amino acids.

Certain peptide or protein sequences longer than 600 amino acids are within the scope of the invention. Such longer sequences are within the scope of the invention so long as they do not comprise any contiguous sequence of more than 600 amino acids that have 100% identity with a native peptide sequence, or if longer than 600 amino acids, they are a construct. For any peptide that has five contiguous residues or less that correspond to a native sequence, there is no limitation on the maximal length of that peptide in order to fall within the scope of the invention. It is presently preferred that a CTL epitope of the invention be less than 600 residues long in any increment down to eight amino acid residues.

"Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (*see, e.g.*, Stites, *et al.*, IMMUNOLOGY, 8TH ED., Lange Publishing, Los Altos, CA, 1994).

An "HLA supertype or family", as used herein, describes sets of HLA molecules grouped on the basis of shared peptide-binding specificities. HLA class I molecules that share somewhat similar binding affinity for peptides bearing certain amino acid motifs are grouped into HLA supertypes. The terms HLA superfamily, HLA supertype family, HLA family, and HLA xx-like molecules (where xx denotes a particular HLA type), are synonyms.

Throughout this disclosure, results are expressed in terms of "IC_{50}'s." IC_{50} is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.*, limiting HLA proteins and labeled peptide concentrations), these values approximate K_D values. Assays for determining binding are described in detail, *e.g.*, in PCT publications WO 94/20127 and WO 94/03205. It should be noted that IC_{50} values can change, often

dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g.*, HLA preparation, *etc.*). For example, excessive concentrations of HLA molecules will increase the apparent measured IC_{50} of a given ligand.

Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC_{50}'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC_{50} of the reference peptide increases 10-fold, the IC_{50} values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good, intermediate, weak, or negative binder is generally based on its IC_{50}, relative to the IC_{50} of a standard peptide.

Binding may also be determined using other assay systems including those using: live cells (*e.g.*, Ceppellini *et al.*, *Nature* 339:392, 1989; Christnick *et al.*, *Nature* 352:67, 1991; Busch *et al.*, *Int. Immunol.* 2:443, 19990; Hill *et al.*, *J. Immunol.* 147:189, 1991; del Guercio *et al.*, *J. Immunol.* 154:685, 1995), cell free systems using detergent lysates (*e.g.*, Cerundolo *et al.*, *J. Immunol.* 21:2069, 1991), immobilized purified MHC (*e.g.*, Hill *et al.*, *J. Immunol.* 152, 2890, 1994; Marshall *et al.*, *J. Immunol.* 152:4946, 1994), ELISA systems (*e.g.*, Reay *et al.*, *EMBO J.* 11:2829, 1992), surface plasmon resonance (*e.g.*, Khilko *et al.*, *J. Biol. Chem.* 268:15425, 1993); high flux soluble phase assays (Hammer *et al.*, *J. Exp. Med.* 180:2353, 1994), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, *Nature* 346:476, 1990; Schumacher *et al.*, *Cell* 62:563, 1990; Townsend *et al.*, *Cell* 62:285, 1990; Parker *et al.*, *J. Immunol.* 149:1896, 1992).

As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC_{50}, or K_D value, of 50 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 50 and about 500 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or K_D value of 100 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 100 and about 1000 nM.

The terms "identical" or percent "identity," in the context of two or more peptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection.

An "immunogenic peptide" or "peptide epitope" is a peptide that comprises an allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL and/or HTL response. Thus, immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and thereafter inducing an HLA-restricted cytotoxic or helper T cell response to the antigen from which the immunogenic peptide is derived.

The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment.

"Link" or "join" refers to any method known in the art for functionally connecting peptides, including, without limitation, recombinant fusion, covalent bonding, disulfide bonding, ionic bonding, hydrogen bonding, and electrostatic bonding.

"Major Histocompatibility Complex" or "MHC" is a cluster of genes that plays a role in control of the cellular interactions responsible for physiologic immune responses. In humans, the MHC complex is also known as the HLA complex. For a detailed description of the MHC and HLA complexes, see, Paul, FUNDAMENTAL IMMUNOLOGY, 3RD ED., Raven Press, New York, 1993.

The term "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids, often 8 to 11 amino acids, for a class I HLA motif and from about 6 to about 25 amino acids for a class II HLA motif, which is recognized by a particular HLA molecule. Peptide motifs are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues.

A "negative binding residue" or "deleterious residue" is an amino acid which, if present at certain positions (typically not primary anchor positions) in a peptide epitope, results in decreased binding affinity of the peptide for the peptide's corresponding HLA molecule.

A "non-native" sequence or "construct" refers to a sequence that is not found in nature, *i.e.*, is "non-naturally occurring". Such sequences include, *e.g.*, peptides that are lipidated or otherwise modified, and polyepitopic compositions that contain epitopes that are not contiguous in a native protein sequence.

The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α-amino and carboxyl groups of adjacent amino acids. CTL-inducing peptides of the invention are often 13 residues or less in length and usually consist of between about 8 and about 11 residues, preferably 9 or 10 residues. HTL-inducing oligopeptides are often less than about 50 residues in length and usually consist of between about 6 and about 30 residues, more usually between about 12 and 25, and often between about 15 and 20 residues.

"Pharmaceutically acceptable" refers to a generally non-toxic, inert, and/or physiologically compatible composition.

A "pharmaceutical excipient" comprises a material such as an adjuvant, a carrier, pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservative, and the like.

A "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One to three, usually two, primary anchor residues within a peptide of defined length generally defines a "motif" for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding grooves of an HLA molecule, with their side chains buried in specific pockets of the binding grooves themselves. In one embodiment, for example, the primary anchor residues are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a 9-residue peptide epitope in accordance with the invention. The primary anchor positions for each motif and supermotif are set forth in Table I. For example, analog peptides can be created by altering the presence or absence of particular residues in these primary anchor positions. Such analogs are used to modulate the binding affinity of a peptide comprising a particular motif or supermotif.

"Promiscuous recognition" is where a distinct peptide is recognized by the same T cell clone in the context of various HLA molecules. Promiscuous recognition or binding is synonymous with cross-reactive binding.

A "protective immune response" or "therapeutic immune response" refers to a CTL and/or an HTL response to an antigen derived from an infectious agent or a tumor antigen, which prevents or at least partially arrests disease symptoms or progression. The immune response may also include an antibody response which has been facilitated by the stimulation of helper T cells.

The term "residue" refers to an amino acid or amino acid mimetic incorporated into an oligopeptide by an amide bond or amide bond mimetic.

A "secondary anchor residue" is an amino acid at a position other than a primary anchor position in a peptide which may influence peptide binding. A secondary anchor residue occurs at a significantly higher frequency amongst bound peptides than would be expected by random distribution of amino acids at one position. The secondary anchor residues are said to occur at "secondary anchor positions." A secondary anchor residue can be identified as a residue which is present at a higher frequency among high or intermediate affinity binding peptides, or a residue otherwise associated with high or intermediate affinity binding. For example, analog peptides can be created by altering the presence or absence of particular residues in these secondary anchor positions. Such analogs are used to finely modulate the binding affinity of a peptide comprising a particular motif or supermotif.

A "subdominant epitope" is an epitope which evokes little or no response upon immunization with whole antigens which comprise the epitope, but for which a response can be obtained by immunization with an isolated peptide, and this response (unlike the case of cryptic epitopes) is detected when whole protein is used to recall the response *in vitro* or *in vivo*.

A "supermotif" is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Preferably, a supermotif-bearing peptide is recognized with high or intermediate affinity (as defined herein) by two or more HLA molecules.

"Synthetic peptide" refers to a peptide that is man-made using such methods as chemical synthesis or recombinant DNA technology.

As used herein, a "vaccine" is a composition that contains one or more peptides of the invention. There are numerous embodiments of vaccines in accordance with the invention, such as by a cocktail of one or more peptides; one or more epitopes of the invention comprised by a polyepitopic peptide; or nucleic acids that encode such peptides or polypeptides, *e.g.*, a minigene that encodes a polyepitopic peptide. The "one or more peptides" can include any whole unit integer from 1-150, *e.g.*, at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40 , 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 or more peptides of the invention. The peptides or polypeptides can optionally be modified, such as by lipidation, addition of

targeting or other sequences. HLA class I-binding peptides of the invention can be admixed with, or linked to, HLA class II-binding peptides, to facilitate activation of both cytotoxic T lymphocytes and helper T lymphocytes. Vaccines can also comprise peptide-pulsed antigen presenting cells, *e.g.*, dendritic cells.

The nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in a peptide epitope they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal end of the epitope, or the peptide or protein of which it may be a part. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G. Symbols for the amino acids are shown below. In addition to these symbols, "B"in the single letter abbreviations used herein designates α-amino butyric acid.

Single Letter Symbol	Three Letter Symbol	Amino Acids
A	Ala	Alanine
C	Cys	Cysteine
D	Asp	Aspartic Acid
E	Glu	Glutamic Acid
F	Phe	Phenylalanine
G	Gly	Glycine
H	His	Histidine
I	Ile	Isoleucine
K	Lys	Lysine
L	Leu	Leucine
M	Met	Methionine
N	Asn	Asparagine
P	Pro	Proline
Q	Gln	Glutamine
R	Arg	Arginine
S	Ser	Serine
T	Thr	Threonine
V	Val	Valine
W	Trp	Tryptophan
Y	Tyr	Tyrosine

IV.B. Stimulation of CTL and HTL responses

The mechanism by which T cells recognize antigens has been delineated during the past ten years. Based on our understanding of the immune system we have developed efficacious peptide epitope vaccine compositions that can induce a therapeutic or prophylactic immune response to a TAA in a broad population. For an understanding of the value and efficacy of the claimed compositions, a brief review of immunology-related technology is provided.

A complex of an HLA molecule and a peptidic antigen acts as the ligand recognized by HLA-restricted T cells (Buus, S. *et al.*, *Cell* 47:1071, 1986; Babbitt, B. P. *et al.*, *Nature* 317:359, 1985; Townsend, A. and Bodmer, H., *Annu. Rev. Immunol.* 7:601,

1989; Germain, R. N., *Annu. Rev. Immunol.* 11:403, 1993). Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues that correspond to motifs required for specific binding to HLA antigen molecules have been identified and are described herein and are set forth in Tables I, II, and III (*see* also, *e.g.*, Southwood, *et al.*, *J. Immunol.* 160:3363, 1998; Rammensee, *et al.*, *Immunogenetics* 41:178, 1995; Rammensee *et al.*, SYFPEITHI, access via web at : http://134.2.96.221/scripts.hlaserver.dll/home.htm; Sette, A. and Sidney, J. *Curr. Opin. Immunol.* 10:478, 1998; Engelhard, V. H., *Curr. Opin. Immunol.* 6:13, 1994; Sette, A. and Grey, H. M., *Curr. Opin. Immunol.* 4:79, 1992; Sinigaglia, F. and Hammer, J. *Curr. Biol.* 6:52, 1994; Ruppert *et al.*, *Cell* 74:929-937, 1993; Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; Sidney *et al.*, *J. Immunol.* 157:3480-3490, 1996; Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; Sette, A. and Sidney, J. *Immunogenetics*, in press, 1999).

Furthermore, x-ray crystallographic analysis of HLA-peptide complexes has revealed pockets within the peptide binding cleft of HLA molecules which accommodate, in an allele-specific mode, residues borne by peptide ligands; these residues in turn determine the HLA binding capacity of the peptides in which they are present. (*See, e.g.*, Madden, D.R. *Annu. Rev. Immunol.* 13:587, 1995; Smith, *et al.*, *Immunity* 4:203, 1996; Fremont *et al.*, *Immunity* 8:305, 1998; Stern *et al.*, *Structure* 2:245, 1994; Jones, E.Y. *Curr. Opin. Immunol.* 9:75, 1997; Brown, J. H. *et al.*, *Nature* 364:33, 1993; Guo, H. C. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:8053, 1993; Guo, H. C. *et al.*, *Nature* 360:364, 1992; Silver, M. L. *et al.*, *Nature* 360:367, 1992; Matsumura, M. *et al.*, *Science* 257:927, 1992; Madden *et al.*, *Cell* 70:1035, 1992; Fremont, D. H. *et al.*, *Science* 257:919, 1992; Saper, M. A. , Bjorkman, P. J. and Wiley, D. C., *J. Mol. Biol.* 219:277, 1991.)

Accordingly, the definition of class I and class II allele-specific HLA binding motifs, or class I or class II supermotifs allows identification of regions within a protein that have the potential of binding particular HLA molecules.

The present inventors have found that the correlation of binding affinity with immunogenicity, which is disclosed herein, is an important factor to be considered when evaluating candidate peptides. Thus, by a combination of motif searches and HLA-peptide binding assays, candidates for epitope-based vaccines have been identified. After determining their binding affinity, additional confirmatory work can be performed to

select, amongst these vaccine candidates, epitopes with preferred characteristics in terms of population coverage, antigenicity, and immunogenicity.

Various strategies can be utilized to evaluate immunogenicity, including:

1) Evaluation of primary T cell cultures from normal individuals (*see, e.g.*, Wentworth, P. A. *et al.*, *Mol. Immunol.* 32:603, 1995; Celis, E. *et al.*, *Proc. Natl. Acad. Sci. USA* 91:2105, 1994; Tsai, V. *et al.*, *J. Immunol.* 158:1796, 1997; Kawashima, I. *et al.*, *Human Immunol.* 59:1, 1998); This procedure involves the stimulation of peripheral blood lymphocytes (PBL) from normal subjects with a test peptide in the presence of antigen presenting cells *in vitro* over a period of several weeks. T cells specific for the peptide become activated during this time and are detected using, *e.g.*, a lymphokine-release or a ^{51}Cr cytotoxicity assay involving peptide sensitized target cells.

2) Immunization of HLA transgenic mice (*see, e.g.*, Wentworth, P. A. *et al.*, *J. Immunol.* 26:97, 1996; Wentworth, P. A. *et al.*, *Int. Immunol.* 8:651, 1996; Alexander, J. *et al.*, *J. Immunol.* 159:4753, 1997); In this method, peptides in incomplete Freund's adjuvant are administered subcutaneously to HLA transgenic mice. Several weeks following immunization, splenocytes are removed and cultured *in vitro* in the presence of test peptide for approximately one week. Peptide-specific T cells are detected using, *e.g.*, a ^{51}Cr-release assay involving peptide sensitized target cells and target cells expressing endogenously generated antigen.

3) Demonstration of recall T cell responses from patients who have been effectively vaccinated or who have a tumor; (*see, e.g.*, Rehermann, B. *et al.*, *J. Exp. Med.* 181:1047, 1995; Doolan, D. L. *et al.*, *Immunity* 7:97, 1997; Bertoni, R. *et al.*, *J. Clin. Invest.* 100:503, 1997; Threlkeld, S. C. *et al.*, *J. Immunol.* 159:1648, 1997; Diepolder, H. M. *et al.*, *J. Virol.* 71:6011, 1997; Tsang *et al.*, *J. Natl. Cancer Inst.* 87:982-990, 1995; Disis *et al.*, *J. Immunol.* 156:3151-3158, 1996). In applying this strategy, recall responses are detected by culturing PBL from patients with cancer who have generated an immune response "naturally", or from patients who were vaccinated with tumor antigen vaccines. PBL from subjects are cultured *in vitro* for 1-2 weeks in the presence of test peptide plus antigen presenting cells (APC) to allow activation of "memory" T cells, as compared to "naive" T cells. At the end of the culture period, T cell activity is detected using assays for T cell activity including ^{51}Cr release involving peptide-sensitized targets, T cell proliferation, or lymphokine release.

The following describes the peptide epitopes and corresponding nucleic acids of the invention.

IV.C. Binding Affinity of Peptide Epitopes for HLA Molecules

As indicated herein, the large degree of HLA polymorphism is an important factor to be taken into account with the epitope-based approach to vaccine development. To address this factor, epitope selection encompassing identification of peptides capable of binding at high or intermediate affinity to multiple HLA molecules is preferably utilized, most preferably these epitopes bind at high or intermediate affinity to two or more allele-specific HLA molecules.

CTL-inducing peptides of interest for vaccine compositions preferably include those that have an IC_{50} or binding affinity value for class I HLA molecules of 500 nM or better (*i.e.*, the value is ≤ 500 nM). HTL-inducing peptides preferably include those that have an IC_{50} or binding affinity value for class II HLA molecules of 1000 nM or better, (*i.e.*, the value is ≤ 1,000 nM). For example, peptide binding is assessed by testing the capacity of a candidate peptide to bind to a purified HLA molecule *in vitro*. Peptides exhibiting high or intermediate affinity are then considered for further analysis. Selected peptides are tested on other members of the supertype family. In preferred embodiments, peptides that exhibit cross-reactive binding are then used in cellular screening analyses or vaccines.

High HLA binding affinity is correlated with greater immunogenicity (*see, e.g.*, Sette, *et al., J. Immunol.* 153:5586-5592, 1994; Chen *et al., J. Immunol.* 152:2874-2881, 1994; and Ressing *et al., J. Immunol.* 154:5934-5943, 1995). Greater immunogenicity can be manifested in several different ways. Immunogenicity corresponds to whether an immune response is elicited at all, and to the vigor of any particular response, as well as to the extent of a population in which a response is elicited. For example, a peptide might elicit an immune response in a diverse array of the population, yet in no instance produce a vigorous response. Moreover, higher binding affinity peptides lead to more vigorous immunogenic responses. As a result, less peptide is required to elicit a similar biological effect if a high or intermediate affinity binding peptide is used. Thus, in preferred embodiments of the invention, high or intermediate affinity binding epitopes are particularly useful.

The relationship between binding affinity for HLA class I molecules and immunogenicity of discrete peptide epitopes on bound antigens has been determined for the first time in the art by the present inventors. The correlation between binding affinity and immunogenicity was analyzed in two different experimental approaches (*see, e.g.*, Sette, *et al., J. Immunol.* 153:5586-5592, 1994). In the first approach, the immunogenicity of potential epitopes ranging in HLA binding affinity over a 10,000-fold range was analyzed in HLA-A*0201 transgenic mice. In the second approach, the antigenicity of approximately 100 different hepatitis B virus (HBV)-derived potential epitopes, all carrying A*0201 binding motifs, was assessed by using PBL from acute hepatitis patients. Pursuant to these approaches, it was determined that an affinity threshold value of approximately 500 nM (preferably 50 nM or less) determines the capacity of a peptide epitope to elicit a CTL response. These data are true for class I binding affinity measurements for naturally processed peptides and for synthesized T cell epitopes. These data also indicate the important role of determinant selection in the shaping of T cell responses (*see, e.g.,* Schaeffer *et al., Proc. Natl. Acad. Sci. USA* 86:4649-4653, 1989).

An affinity threshold associated with immunogenicity in the context of HLA class II DR molecules has also been delineated (*see, e.g.*, Southwood *et al. J. Immunology* 160:3363-3373,1998, and co-pending U.S.S.N. 09/009,953 filed 1/21/98). In order to define a biologically significant threshold of DR binding affinity, a database of the binding affinities of 32 DR-restricted epitopes for their restricting element (*i.e.*, the HLA molecule that binds the motif) was compiled. In approximately half of the cases (15 of 32 epitopes), DR restriction was associated with high binding affinities, *i.e.* binding affinity values of 100 nM or less. In the other half of the cases (16 of 32), DR restriction was associated with intermediate affinity (binding affinity values in the 100-1000 nM range). In only one of 32 cases was DR restriction associated with an IC_{50} of 1000 nM or greater. Thus, 1000 nM can be defined as an affinity threshold associated with immunogenicity in the context of DR molecules.

In the case of tumor-associated antigens, many CTL peptide epitopes that have been shown to induce CTL that lyse peptide-pulsed target cells and tumor cell targets endogenously expressing the epitope exhibit binding affinity or IC_{50} values of 200 nM or less. In a study that evaluated the association of binding affinity and immunogenicity of a small set of such TAA epitopes, 100% (10/10) of the high binders, *i.e.*, peptide epitopes binding at an affinity of 50 nM or less, were immunogenic and 80%

(8/10) of them elicited CTLs that specifically recognized tumor cells. In the 51 to 200 nM range, very similar figures were obtained. With respect to analog peptides, CTL inductions positive for wildtype peptide and tumor cells were noted for 86% (6/7) and 71% (5/7) of the peptides, respectively. In the 201-500 nM range, most peptides (4/5 wildtype) were positive for induction of CTL recognizing wildtype peptide, but tumor recognition was not detected.

The binding affinity of peptides for HLA molecules can be determined as described in Example 1, below.

IV.D. Peptide Epitope Binding Motifs and Supermotifs

Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues required for allele-specific binding to HLA molecules have been identified. The presence of these residues correlates with binding affinity for HLA molecules. The identification of motifs and/or supermotifs that correlate with high and intermediate affinity binding is an important issue with respect to the identification of immunogenic peptide epitopes for the inclusion in a vaccine. Kast *et al.* (*J. Immunol.* 152:3904-3912, 1994) have shown that motif-bearing peptides account for 90% of the epitopes that bind to allele-specific HLA class I molecules. In this study all possible peptides of 9 amino acids in length and overlapping by eight amino acids (240 peptides), which cover the entire sequence of the E6 and E7 proteins of human papillomavirus type 16, were evaluated for binding to five allele-specific HLA molecules that are expressed at high frequency among different ethnic groups. This unbiased set of peptides allowed an evaluation of the predictive value of HLA class I motifs. From the set of 240 peptides, 22 peptides were identified that bound to an allele-specific HLA molecule with high or intermediate affinity. Of these 22 peptides, 20 (*i.e.* 91%) were motif-bearing. Thus, this study demonstrates the value of motifs for the identification of peptide epitopes for inclusion in a vaccine: application of motif-based identification techniques will identify about 90% of the potential epitopes in a target antigen protein sequence.

Such peptide epitopes are identified in the Tables described below.

Peptides of the present invention may also comprise epitopes that bind to MHC class II DR molecules. A greater degree of heterogeneity in both size and binding frame position of the motif, relative to the N and C termini of the peptide, exists for class II peptide ligands. This increased heterogeneity of HLA class II peptide ligands is due to

the structure of the binding groove of the HLA class II molecule which, unlike its class I counterpart, is open at both ends. Crystallographic analysis of HLA class II DRB*0101-peptide complexes showed that the major energy of binding is contributed by peptide residues complexed with complementary pockets on the DRB*0101 molecules. An important anchor residue engages the deepest hydrophobic pocket (*see, e.g.*, Madden, D.R. *Ann. Rev. Immunol.* 13:587, 1995) and is referred to as position 1 (P1). P1 may represent the N-terminal residue of a class II binding peptide epitope, but more typically is flanked towards the N-terminus by one or more residues. Other studies have also pointed to an important role for the peptide residue in the 6th position towards the C-terminus, relative to P1, for binding to various DR molecules.

In the past few years evidence has accumulated to demonstrate that a large fraction of HLA class I and class II molecules can be classified into a relatively few supertypes, each characterized by largely overlapping peptide binding repertoires, and consensus structures of the main peptide binding pockets. Thus, peptides of the present invention are identified by any one of several HLA-specific amino acid motifs (*see, e.g.*, Tables I-III), or if the presence of the motif corresponds to the ability to bind several allele-specific HLA molecules, a supermotif. The HLA molecules that bind to peptides that possess a particular amino acid supermotif are collectively referred to as an HLA "supertype."

The peptide motifs and supermotifs described below, and summarized in Tables I-III, provide guidance for the identification and use of peptide epitopes in accordance with the invention.

Examples of supermotif and/or motif-bearing peptide epitopes are shown in Tables VII-XX. To obtain the peptide epitope sequences, protein sequence data for the prostate cancer antigens PAP, PSA, PSM, and hK2, which is designated as kallikrein in Tables VII-XX, were evaluated for the presence of the designated supermotif or motif. The "Position" column indicates the position in the protein sequence that corresponds to the first amino acid residue of the putative epitope. The "number of amino acids" indicates the number of residues in the epitope sequence. The tables also include a binding affinity ratio listing for some of the peptide epitopes for the allele-specific HLA molecule indicated in the column heading. The ratio may be converted to IC_{50} by using the following formula: IC_{50} of the standard peptide/ratio = IC_{50} of the test peptide (*i.e.*, the peptide epitope). The IC_{50} values of standard peptides used to determine binding affinities for Class I peptides are shown in Table IV. The IC_{50} values of standard peptides

used to determine binding affinities for Class II peptides are shown in Table V. The peptides used as standards for the binding assays described herein are examples of standards; alternative standard peptides can also be used when performing binding studies.

HLA Class I Motifs Indicative of CTL Inducing Peptide Epitopes:

The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs delineated below are summarized in Table I. The HLA class I motifs set out in Table I(a) are those most particularly relevant to the invention claimed here. Primary and secondary anchor positions are summarized in Table II. Allele-specific HLA molecules that comprise HLA class I supertype families are listed in Table VI. In some cases, peptide epitopes may be listed in both a motif and a supermotif Table. The relationship of a particular motif and respective supermotif is indicated in the description of the individual motifs.

IV.D.1. HLA-A1 supermotif

The HLA-A1 supermotif is characterized by the presence in peptide ligands of a small (T or S) or hydrophobic (L, I, V, or M) primary anchor residue in position 2, and an aromatic (Y, F, or W) primary anchor residue at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind to the A1 supermotif (*i.e.*, the HLA-A1 supertype) is comprised of at least: A*0101, A*2601, A*2602, A*2501, and A*3201 (*see, e.g.*, DiBrino, M. *et al.*, *J. Immunol.* 151:5930, 1993; DiBrino, M. *et al.*, *J. Immunol.* 152:620, 1994; Kondo, A. *et al.*, *Immunogenetics* 45:249, 1997). Other allele-specific HLA molecules predicted to be members of the A1 superfamily are shown in Table VI. Peptides binding to each of the individual HLA proteins can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise an A1 supermotif are set forth on the attached Table VII.

IV.D.2. HLA-A2 supermotif

Primary anchor specificities for allele-specific HLA-A2.1 molecules (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991; Hunt *et al.*, *Science* 255:1261-1263, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992; Ruppert *et al.*, *Cell* 74:929-937, 1993)

and cross-reactive binding among HLA-A2 and -A28 molecules have been described. (*See, e.g.*, Fruci *et al.*, *Human Immunol.* 38:187-192, 1993; Tanigaki *et al.*, *Human Immunol.* 39:155-162, 1994; Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994 for reviews of relevant data.) These primary anchor residues define the HLA-A2 supermotif; which presence in peptide ligands corresponds to the ability to bind several different HLA-A2 and -A28 molecules. The HLA-A2 supermotif comprises peptide ligands with L, I, V, M, A, T, or Q as a primary anchor residue at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope.

The corresponding family of HLA molecules (*i.e.*, the HLA-A2 supertype that binds these peptides) is comprised of at least: A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, and A*6901. Other allele-specific HLA molecules predicted to be members of the A2 superfamily are shown in Table VI. As explained in detail below, binding to each of the individual allele-specific HLA molecules can be modulated by substitutions at the primary anchor and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise an A2 supermotif are set forth on the attached Table VIII. The motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

IV.D.3. HLA-A3 supermotif

The HLA-A3 supermotif is characterized by the presence in peptide ligands of A, L, I, V, M, S, or, T as a primary anchor at position 2, and a positively charged residue, R or K, at the C-terminal position of the epitope, *e.g.*, in position 9 of 9-mers (*see, e.g.*, Sidney *et al.*, *Hum. Immunol.* 45:79, 1996). Exemplary members of the corresponding family of HLA molecules (the HLA-A3 supertype) that bind the A3 supermotif include at least: A*0301, A*1101, A*3101, A*3301, and A*6801. Other allele-specific HLA molecules predicted to be members of the A3 supertype are shown in Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions of amino acids at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A3 supermotif are set forth on the attached Table IX.

IV.D.4. HLA-A24 supermotif

The HLA-A24 supermotif is characterized by the presence in peptide ligands of an aromatic (F, W, or Y) or hydrophobic aliphatic (L, I, V, M, or T) residue as a primary anchor in position 2, and Y, F, W, L, I, or M as primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sette and Sidney, *Immunogenetics*, in press, 1999). The corresponding family of HLA molecules that bind to the A24 supermotif (*i.e.*, the A24 supertype) includes at least: A*2402, A*3001, and A*2301. Other allele-specific HLA molecules predicted to be members of the A24 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A24 supermotif are set forth on the attached Table X.

IV.D.5. HLA-B7 supermotif

The HLA-B7 supermotif is characterized by peptides bearing proline in position 2 as a primary anchor, and a hydrophobic or aliphatic amino acid (L, I, V, M, A, F, W, or Y) as the primary anchor at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind the B7 supermotif (*i.e.*, the HLA-B7 supertype) is comprised of at least twenty six HLA-B proteins comprising at least: B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, and B*7801 (*see, e.g.*, Sidney, *et al., J. Immunol.* 154:247, 1995; Barber, *et al., Curr. Biol.* 5:179, 1995; Hill, *et al., Nature* 360:434, 1992; Rammensee, *et al., Immunogenetics* 41:178, 1995 for reviews of relevant data). Other allele-specific HLA molecules predicted to be members of the B7 supertype are shown in Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B7 supermotif are set forth on the attached Table XI.

IV.D.6. HLA-B27 supermotif

The HLA-B27 supermotif is characterized by the presence in peptide ligands of a positively charged (R, H, or K) residue as a primary anchor at position 2, and a hydrophobic (F, Y, L, W, M, I, A, or V) residue as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B27 supermotif (*i.e.*, the B27 supertype) include at least B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, and B*7301. Other allele-specific HLA molecules predicted to be members of the B27 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B27 supermotif are set forth on the attached Table XII.

IV.D.7. HLA-B44 supermotif

The HLA-B44 supermotif is characterized by the presence in peptide ligands of negatively charged (D or E) residues as a primary anchor in position 2, and hydrophobic residues (F, W, Y, L, I, M, V, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney et al., *Immunol. Today* 17:261, 1996). Exemplary members of the corresponding family of HLA molecules that bind to the B44 supermotif (*i.e.*, the B44 supertype) include at least: B*1801, B*1802, B*3701, B*4001, B*4002, B*4006, B*4402, B*4403, and B*4404. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the supermotif.

IV.D.8. HLA-B58 supermotif

The HLA-B58 supermotif is characterized by the presence in peptide ligands of a small aliphatic residue (A, S, or T) as a primary anchor residue at position 2, and an aromatic or hydrophobic residue (F, W, Y, L, I, V, M, or A) as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette,

Immunogenetics, in press, 1999 for reviews of relevant data). Exemplary members of the corresponding family of HLA molecules that bind to the B58 supermotif (*i.e.*, the B58 supertype) include at least: B*1516, B*1517, B*5701, B*5702, and B*5801. Other allele-specific HLA molecules predicted to be members of the B58 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B27 supermotif are set forth on the attached Table XII.

IV.D.9. HLA-B62 supermotif

The HLA-B62 supermotif is characterized by the presence in peptide ligands of the polar aliphatic residue Q or a hydrophobic aliphatic residue (L, V, M, I, or P) as a primary anchor in position 2, and a hydrophobic residue (F, W, Y, M, I, V, L, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B62 supermotif (*i.e.*, the B62 supertype) include at least: B*1501, B*1502, B*1513, and B5201. Other allele-specific HLA molecules predicted to be members of the B62 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B62 supermotif are set forth on the attached Table XIV.

IV.D.10. HLA-A1 motif

The HLA-A1 motif is characterized by the presence in peptide ligands of T, S, or M as a primary anchor residue at position 2 and the presence of Y as a primary anchor residue at the C-terminal position of the epitope. An alternative allele-specific A1 motif is characterized by a primary anchor residue at position 3 rather than position 2. This motif is characterized by the presence of D, E, A, or S as a primary anchor residue in position 3, and a Y as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, DiBrino *et al.*, J. Immunol., 152:620, 1994; Kondo *et al.*, *Immunogenetics* 45:249, 1997; and Kubo *et al.*, *J. Immunol.* 152:3913, 1994 for reviews of relevant data).

Peptide binding to HLA-A1 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise either A1 motif are set forth on the attached Table XV. Those epitopes comprising T, S, or M at position 2 and Y at the C-terminal position are also included in the listing of HLA-A1 supermotif-bearing peptide epitopes listed in Table VII, as these residues are a subset of the A1 supermotif.

IV.D.11. HLA-A*0201 motif

An HLA-A2*0201 motif was determined to be characterized by the presence in peptide ligands of L or M as a primary anchor residue in position 2, and L or V as a primary anchor residue at the C-terminal position of a 9-residue peptide (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991) and was further found to comprise an I at position 2 and I or A at the C-terminal position of a nine amino acid peptide (*see, e.g.*, Hunt *et al.*, Science 255:1261-1263, March 6, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992). The A*0201 allele-specific motif has also been defined by the present inventors to additionally comprise V, A, T, or Q as a primary anchor residue at position 2, and M or T as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994). Thus, the HLA-A*0201 motif comprises peptide ligands with L, I, V, M, A, T, or Q as primary anchor residues at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope. The preferred and tolerated residues that characterize the primary anchor positions of the HLA-A*0201 motif are identical to the residues describing the A2 supermotif. (For reviews of relevant data, *see, e.g.*, del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Ruppert *et al.*, *Cell* 74:929-937, 1993; Sidney *et al.*, *Immunol. Today* 17:261-266, 1996; Sette and Sidney, *Curr. Opin. in Immunol.* 10:478-482, 1998). Secondary anchor residues that characterize the A*0201 motif have additionally been defined (*see, e.g.*, Ruppert *et al.*, *Cell* 74:929-937, 1993). These are shown in Table II. Peptide binding to HLA-A*0201 molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise an A*0201 motif are set forth on the attached Table VII. The A*0201 motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

IV.D.12. HLA-A3 motif

The HLA-A3 motif is characterized by the presence in peptide ligands of L, M, V, I, S, A, T, F, C, G, or D as a primary anchor residue at position 2, and the presence of K, Y, R, H, F, or A as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, DiBrino *et al.*, *Proc. Natl. Acad. Sci USA* 90:1508, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A3 motif are set forth on the attached Table XVI. Those epitopes that comprise the A3 supermotif are also listed in Table IX, as the A3 supermotif primary anchor residues comprise a subset of the A3- and A11-allele-specific motifs.

IV.D.13. HLA-A11 motif

The HLA-A11 motif is characterized by the presence in peptide ligands of V, T, M, L, I, S, A, G, N, C, D, or F as a primary anchor residue in position 2, and K, R, Y, or H as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, Zhang *et al.*, *Proc. Natl. Acad. Sci USA* 90:2217-2221, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A11 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A11 motif are set forth on the attached Table XVII; peptide epitopes comprising the A3 allele-specific motif are also present in this Table because of the extensive overlap between the A3 and A11 motif primary anchor specificities. Further, those peptide epitopes that comprise the A3 supermotif are also listed in Table IX.

IV.D.14. HLA-A24 motif

The HLA-A24 motif is characterized by the presence in peptide ligands of Y, F, W, or M as a primary anchor residue in position 2, and F, L, I, or W as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.*, *Kondo et al.*, *J. Immunol.* 155:4307-4312, 1995; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A24 molecules can be modulated by substitutions at primary

and/or secondary anchor positions; preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A24 motif are set forth on the attached Table XVIII. These epitopes are also listed in Table X, which sets forth HLA-A24-supermotif-bearing peptide epitopes, as the primary anchor residues characterizing the A24 allele-specific motif comprise a subset of the A24 supermotif primary anchor residues.

Motifs Indicative of Class II HTL Inducing Peptide Epitopes

The primary and secondary anchor residues of the HLA class II peptide epitope supermotifs and motifs delineated below are summarized in Table III.

IV.D.15. HLA DR-1-4-7 supermotif

Motifs have also been identified for peptides that bind to three common HLA class II allele-specific HLA molecules: HLA DRB1*0401, DRB1*0101, and DRB1*0701 (*see, e.g.*, the review by Southwood *et al. J. Immunology* 160:3363-3373,1998). Collectively, the common residues from these motifs delineate the HLA DR-1-4-7 supermotif. Peptides that bind to these DR molecules carry a supermotif characterized by a large aromatic or hydrophobic residue (Y, F, W, L, I, V, or M) as a primary anchor residue in position 1, and a small, non-charged residue (S, T, C, A, P, V, I, L, or M) as a primary anchor residue in position 6 of a 9-mer core region. Allele-specific secondary effects and secondary anchors for each of these HLA types have also been identified (Southwood *et al., supra*). These are set forth in Table III. Peptide binding to HLA- DRB1*0401, DRB1*0101, and/or DRB1*0701 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative 9-mer epitopes comprising the DR-1-4-7 supermotif, wherein position 1 of the supermotif is at position 1 of the nine-residue core, are set forth in Table XIX. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in the Table.

IV.D.16. HLA-DR3 motifs

Two alternative motifs (*i.e.*, submotifs) characterize peptide epitopes that bind to HLA-DR3 molecules (*see, e.g.*, Geluk *et al.*, *J. Immunol.* 152:5742, 1994). In the first motif (submotif DR3a) a large, hydrophobic residue (L, I, V, M, F, or Y) is present in anchor position 1 of a 9-mer core, and D is present as an anchor at position 4, towards the carboxyl terminus of the epitope. As in other class II motifs, core position 1 may or may not occupy the peptide N-terminal position.

The alternative DR3 submotif provides for lack of the large, hydrophobic residue at anchor position 1, and/or lack of the negatively charged or amide-like anchor residue at position 4, by the presence of a positive charge at position 6 towards the carboxyl terminus of the epitope. Thus, for the alternative allele-specific DR3 motif (submotif DR3b): L, I, V, M, F, Y, A, or Y is present at anchor position 1; D, N, Q, E, S, or T is present at anchor position 4; and K, R, or H is present at anchor position 6. Peptide binding to HLA-DR3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Peptide epitope 9-mer core regions corresponding to a nine residue sequence comprising the DR3a or the DR3b submotifs (wherein position 1 of the motif is at position 1 of the nine residue core) are set forth in Table XXa and b. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in Table XX.

Each of the HLA class I or class II peptide epitopes identified as described herein is deemed singly to be an inventive aspect of this application. Further, it is also an inventive aspect of this application that each peptide epitope may be used in combination with any other peptide epitope.

IV.E. Enhancing Population Coverage of the Vaccine

Vaccines that have broad population coverage are preferred because they are more commercially viable and generally applicable to the most people. Broad population coverage can be obtained using the peptides of the invention (and/or nucleic acid compositions that encode such peptides) through selecting peptide epitopes that bind to HLA alleles which, when considered in total, are present in most of the population. Table XXI shows the overall frequencies of HLA class I supertypes in various ethnicities (Table XXIa) and the combined population coverage achieved by the A2-, A3-, and B7-

supertypes (Table XXIb). The A2-, A3-, and B7 supertypes are each present on average of over 40% in each of these five major ethnic groups. Coverage in excess of 80% is achieved with a combination of these supermotifs. These results suggest that effective and non-ethnically biased population coverage is achieved upon use of a limited number of cross-reactive peptides. Although the population coverage reached with these three main peptide specificities is high, coverage can be expanded to reach 95% population coverage and above, and more easily achieve truly multispecific responses upon use of additional supermotif or allele-specific motif bearing peptides.

The B44-, A1-, and A24-supertypes are each present, on average, in a range from 25% to 40% in these major ethnic populations (Table XXIa). While less prevalent overall, the B27-, B58-, and B62 supertypes are each present with a frequency >25% in at least one major ethnic group (Table XXIa). Table XXIb summarizes the estimated prevalence of combinations of HLA supertypes that have been identified in five major ethnic groups; the incremental coverage obtained by the inclusion of A1,- A24-, and B44-supertypes to the A2, A3, and B7 coverage; and coverage obtained with all of the supertypes described herein, is shown.

The data presented herein, together with the previous definition of the A2-, A3-, and B7-supertypes, indicates that all antigens, with the possible exception of A29, B8, and B46, can be classified into a total of nine HLA supertypes. By including epitopes from the six most frequent supertypes, an average population coverage of 99% is obtained for five major ethnic groups.

IV.F. Immune Response-Stimulating Peptide Analogs

In general, CTL and HTL responses to whole antigens are not directed against all possible epitopes. Rather, they are restricted to a few "immunodominant" determinants (Zinkernagel, *et al., Adv. Immunol.* 27:5159, 1979; Bennink, *et al., J. Exp. Med.* 168:19351939, 1988; Rawle, *et al., J. Immunol.* 146:3977-3984, 1991). It has been recognized that immunodominance (Benacerraf, *et al., Science* 175:273-279, 1972) could be explained by either the ability of a given epitope to selectively bind a particular HLA protein (determinant selection theory) (Vitiello, *et al., J. Immunol.* 131:1635, 1983); Rosenthal, *et al., Nature* 267:156-158, 1977), or to be selectively recognized by the existing TCR (T cell receptor) specificities (repertoire theory) (Klein, J., IMMUNOLOGY, THE SCIENCE OF SELF/NONSELF DISCRIMINATION, John Wiley & Sons, New York, pp. 270-310, 1982). It has been demonstrated that additional factors, mostly linked to

processing events, can also play a key role in dictating, beyond strict immunogenicity, which of the many potential determinants will be presented as immunodominant (Sercarz, *et al.*, *Annu. Rev. Immunol.* 11:729-766, 1993).

Because tissue specific and developmental TAAs are expressed on normal tissue at least at some point in time or location within the body, it may be expected that T cells to them, particularly dominant epitopes, are eliminated during immunological surveillance and that tolerance is induced. However, CTL responses to tumor epitopes in both normal donors and cancer patient have been detected, which may indicate that tolerance is incomplete (*see*, *e.g.*, Kawashima *et al.*, Hum. Immunol. 59:1, 1998; Tsang, *J. Natl. Cancer Inst.* 87:82-90, 1995; Rongcun *et al.*, *J. Immunol.* 163:1037, 1999). Thus, immune tolerance does not completely eliminate or inactivate CTL precursors capable of recognizing high affinity HLA class I binding peptides.

An additional strategy to overcome tolerance is to use analog peptides. Without intending to be bound by theory, it is believed that because T cells to dominant epitopes may have been clonally deleted, selecting subdominant epitopes may allow existing T cells to be recruited, which will then lead to a therapeutic or prophylactic response. However, the binding of HLA molecules to subdominant epitopes is often less vigorous than to dominant ones. Accordingly, there is a need to be able to modulate the binding affinity of particular immunogenic epitopes for one or more HLA molecules, and thereby to modulate the immune response elicited by the peptide, for example to prepare analog peptides which elicit a more vigorous response.

Although peptides with suitable cross-reactivity among all alleles of a superfamily are identified by the screening procedures described above, cross-reactivity is not always as complete as possible, and in certain cases procedures to increase cross-reactivity of peptides can be useful; moreover, such procedures can also be used to modify other properties of the peptides such as binding affinity or peptide stability. Having established the general rules that govern cross-reactivity of peptides for HLA alleles within a given motif or supermotif, modification (*i.e.*, analoging) of the structure of peptides of particular interest in order to achieve broader (or otherwise modified) HLA binding capacity can be performed. More specifically, peptides which exhibit the broadest cross-reactivity patterns, can be produced in accordance with the teachings herein. The present concepts related to analog generation are set forth in greater detail in co-pending U.S.S.N. 09/226,775 filed 1/6/99.

In brief, the strategy employed utilizes the motifs or supermotifs which correlate with binding to certain HLA molecules. The motifs or supermotifs are defined by having primary anchors, and in many cases secondary anchors. Analog peptides can be created by substituting amino acid residues at primary anchor, secondary anchor, or at primary and secondary anchor positions. Generally, analogs are made for peptides that already bear a motif or supermotif. Preferred secondary anchor residues of supermotifs and motifs that have been defined for HLA class I and class II binding peptides are shown in Tables II and III, respectively.

For a number of the motifs or supermotifs in accordance with the invention, residues are defined which are deleterious to binding to allele-specific HLA molecules or members of HLA supertypes that bind the respective motif or supermotif (Tables II and III). Accordingly, removal of such residues that are detrimental to binding can be performed in accordance with the present invention. For example, in the case of the A3 supertype, when all peptides that have such deleterious residues are removed from the population of peptides used in the analysis, the incidence of cross-reactivity increased from 22% to 37% (*see, e.g.*, Sidney, J. *et al.*, *Hu. Immunol.* 45:79, 1996). Thus, one strategy to improve the cross-reactivity of peptides within a given supermotif is simply to delete one or more of the deleterious residues present within a peptide and substitute a small "neutral" residue such as Ala (that may not influence T cell recognition of the peptide). An enhanced likelihood of cross-reactivity is expected if, together with elimination of detrimental residues within a peptide, "preferred" residues associated with high affinity binding to an allele-specific HLA molecule or to multiple HLA molecules within a superfamily are inserted.

To ensure that an analog peptide, when used as a vaccine, actually elicits a CTL response to the native epitope *in vivo* (or, in the case of class II epitopes, elicits helper T cells that cross-react with the wild type peptides), the analog peptide may be used to immunize T cells *in vitro* from individuals of the appropriate HLA allele. Thereafter, the immunized cells' capacity to induce lysis of wild type peptide sensitized target cells is evaluated. It will be desirable to use as antigen presenting cells, cells that have been either infected, or transfected with the appropriate genes, or, in the case of class II epitopes, cells that have been pulsed with whole protein antigens, to establish whether endogenously produced antigen is also recognized by the relevant T cells.

Another embodiment of the invention is to create analogs of weak binding peptides, to thereby ensure adequate numbers of cross-reactive cellular binders. Class I

binding peptides exhibiting binding affinities of 500-5000 nM, and carrying an acceptable but suboptimal primary anchor residue at one or both positions can be "fixed" by substituting preferred anchor residues in accordance with the respective supertype. The analog peptides can then be tested for crossbinding activity.

Another embodiment for generating effective peptide analogs involves the substitution of residues that have an adverse impact on peptide stability or solubility in, *e.g.*, a liquid environment. This substitution may occur at any position of the peptide epitope. For example, a cysteine can be substituted out in favor of α-amino butyric acid ("B" in the single letter abbreviations for peptide sequences listed herein). Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substituting α-amino butyric acid for cysteine not only alleviates this problem, but actually improves binding and crossbinding capability in certain instances (*see, e.g.*, the review by Sette *et al.*, In: Persistent Viral Infections, Eds. R. Ahmed and I. Chen, John Wiley & Sons, England, 1999).

IV.G. Computer Screening of Protein Sequences from Disease-Related Antigens for Supermotif- or Motif-Bearing Peptides

In order to identify supermotif- or motif-bearing epitopes in a target antigen, a native protein sequence, *e.g.*, a tumor-associated antigen, or sequences from an infectious organism, or a donor tissue for transplantation, is screened using a means for computing, such as an intellectual calculation or a computer, to determine the presence of a supermotif or motif within the sequence. The information obtained from the analysis of native peptide can be used directly to evaluate the status of the native peptide or may be utilized subsequently to generate the peptide epitope.

Computer programs that allow the rapid screening of protein sequences for the occurrence of the subject supermotifs or motifs are encompassed by the present invention; as are programs that permit the generation of analog peptides. These programs are implemented to analyze any identified amino acid sequence or operate on an unknown sequence and simultaneously determine the sequence and identify motif-bearing epitopes thereof; analogs can be simultaneously determined as well. Generally, the identified sequences will be from a pathogenic organism or a tumor-associated peptide. In the present invention, the target TAA molecules include, without limitation, PSA, PSM, PAP, and hK2.

It is important that the selection criteria utilized for prediction of peptide binding are as accurate as possible, to correlate most efficiently with actual binding. Prediction of peptides that bind, for example, to HLA-A*0201, on the basis of the presence of the appropriate primary anchors, is positive at about a 30% rate (*see, e.g.*, Ruppert, J. *et al. Cell* 74:929, 1993). However, by extensively analyzing peptide-HLA binding data disclosed herein, data in related patent applications, and data in the art, the present inventors have developed a number of allele-specific polynomial algorithms that dramatically increase the predictive value over identification on the basis of the presence of primary anchor residues alone. These algorithms take into account not only the presence or absence of primary anchors, but also consider the positive or deleterious presence of secondary anchor residues (to account for the impact of different amino acids at different positions). The algorithms are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA interactions can be approximated as a linear polynomial function of the type:

$$\Delta G = a_{1i} \times a_{2i} \times a_{3i} \ldots \times a_{ni}$$

where a_{ji} is a coefficient that represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. An important assumption of this method is that the effects at each position are essentially independent of each other. This assumption is justified by studies that demonstrated that peptides are bound to HLA molecules and recognized by T cells in essentially an extended conformation. Derivation of specific algorithm coefficients has been described, for example, in Gulukota, K. *et al., J. Mol. Biol.* 267:1258, 1997.

Additional methods to identify preferred peptide sequences, which also make use of specific motifs, include the use of neural networks and molecular modeling programs (*see, e.g.*, Milik *et al., Nature Biotechnology* 16:753, 1998; Altuvia *et al., Hum. Immunol.* 58:1, 1997; Altuvia *et al, J. Mol. Biol.* 249:244, 1995; Buus, S. *Curr. Opin. Immunol.* 11:209-213, 1999; Brusic, V. *et al., Bioinformatics* 14:121-130, 1998; Parker *et al., J. Immunol.* 152:163, 1993; Meister *et al., Vaccine* 13:581, 1995; Hammer *et al., J. Exp. Med.* 180:2353, 1994; Sturniolo *et al., Nature Biotechnol.* 17:555 1999).

For example, it has been shown that in sets of A*0201 motif-bearing peptides containing at least one preferred secondary anchor residue while avoiding the presence of any deleterious secondary anchor residues, 69% of the peptides will bind A*0201 with an IC_{50} less than 500 nM (Ruppert, J. *et al. Cell* 74:929, 1993). These

algorithms are also flexible in that cut-off scores may be adjusted to select sets of peptides with greater or lower predicted binding properties, as desired.

In utilizing computer screening to identify peptide epitopes, a protein sequence or translated sequence may be analyzed using software developed to search for motifs, for example the "FINDPATTERNS' program (Devereux, *et al. Nucl. Acids Res.* 12:387-395, 1984) or MotifSearch 1.4 software program (D. Brown, San Diego, CA) to identify potential peptide sequences containing appropriate HLA binding motifs. The identified peptides can be scored using customized polynomial algorithms to predict their capacity to bind specific HLA class I or class II alleles. As appreciated by one of ordinary skill in the art, a large array of computer programming software and hardware options are available in the relevant art which can be employed to implement the motifs of the invention in order to evaluate (*e.g.*, without limitation, to identify epitopes, identify epitope concentration per peptide length, or to generate analogs) known or unknown peptide sequences.

In accordance with the procedures described above, prostate cancer-associated antigen peptide epitopes and analogs thereof that are able to bind HLA supertype groups or allele-specific HLA molecules are identified.

IV.H. Preparation of Peptide Epitopes

Peptides in accordance with the invention can be prepared synthetically, by recombinant DNA technology or chemical synthesis, or from natural sources such as native tumors or pathogenic organisms. Peptide epitopes may be synthesized individually or as polyepitopic peptides. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides may be synthetically conjugated to native fragments or particles.

The peptides in accordance with the invention can be a variety of lengths, and either in their neutral (uncharged) forms or in forms which are salts. The peptides in accordance with the invention are either free of modifications such as glycosylation, side chain oxidation, or phosphorylation; or they contain these modifications, subject to the condition that modifications do not destroy the biological activity of the peptides as described herein.

When possible, it may be desirable to optimize HLA class I binding epitopes of the invention, such as can be used in a polyepitopic construct, to a length of about 8 to about 13 amino acid residues, often 8 to 11, preferably 9 to 10. HLA class II

binding peptide epitopes of the invention may be optimized to a length of about 6 to about 30 amino acids in length, preferably to between about 13 and about 20 residues. Preferably, the peptide epitopes are commensurate in size with endogenously processed pathogen-derived peptides or tumor cell peptides that are bound to the relevant HLA molecules, however, the identification and preparation of peptides that comprise epitopes of the invention can also be carried out using the techniques described herein.

In alternative embodiments, epitopes of the invention can be linked as a polyepitopic peptide, or as a minigene that encodes a polyepitopic peptide.

In another embodiment, it is preferred to identify native peptide regions that contain a high concentration of class I and/or class II epitopes. Such a sequence is generally selected on the basis that it contains the greatest number of epitopes per amino acid length. It is to be appreciated that epitopes can be present in a nested or overlapping manner, *e.g.* a 10 amino acid long peptide could contain two 9 amino acid long epitopes and one 10 amino acid long epitope; upon intracellular processing, each epitope can be exposed and bound by an HLA molecule upon administration of such a peptide. This larger, preferably multi-epitopic, peptide can be generated synthetically, recombinantly, or via cleavage from the native source.

The peptides of the invention can be prepared in a wide variety of ways. For the preferred relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. (*See*, for example, Stewart & Young, SOLID PHASE PEPTIDE SYNTHESIS, 2D. ED., Pierce Chemical Co., 1984). Further, individual peptide epitopes can be joined using chemical ligation to produce larger peptides that are still within the bounds of the invention.

Alternatively, recombinant DNA technology can be employed wherein a nucleotide sequence which encodes an immunogenic peptide of interest is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art, as described generally in Sambrook *et al.*, MOLECULAR CLONING, A LABORATORY MANUAL, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989). Thus, recombinant polypeptides which comprise one or more peptide sequences of the invention can be used to present the appropriate T cell epitope.

The nucleotide coding sequence for peptide epitopes of the preferred lengths contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci, *et al., J. Am. Chem. Soc.* 103:3185 (1981). Peptide analogs can be made simply by substituting the appropriate and desired nucleic acid base(s) for those that encode the native peptide sequence; exemplary nucleic acid substitutions are those that encode an amino acid defined by the motifs/supermotifs herein. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired fusion protein. A number of such vectors and suitable host systems are now available. For expression of the fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts. Of course, yeast, insect or mammalian cell hosts may also be used, employing suitable vectors and control sequences.

IV.I. Assays to Detect T-Cell Responses

Once HLA binding peptides are identified, they can be tested for the ability to elicit a T-cell response. The preparation and evaluation of motif-bearing peptides are described in PCT publications WO 94/20127 and WO 94/03205. Briefly, peptides comprising epitopes from a particular antigen are synthesized and tested for their ability to bind to the appropriate HLA proteins. These assays may involve evaluating the binding of a peptide of the invention to purified HLA class I molecules in relation to the binding of a radioiodinated reference peptide. Alternatively, cells expressing empty class I molecules (*i.e.* lacking peptide therein) may be evaluated for peptide binding by immunofluorescent staining and flow microfluorimetry. Other assays that may be used to evaluate peptide binding include peptide-dependent class I assembly assays and/or the inhibition of CTL recognition by peptide competition. Those peptides that bind to the class I molecule, typically with an affinity of 500 nM or less, are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary *in vitro* or *in vivo* CTL responses that can

give rise to CTL populations capable of reacting with selected target cells associated with a disease.

Analogous assays are used for evaluation of HLA class II binding peptides. HLA class II motif-bearing peptides that are shown to bind, typically at an affinity of 1000 nM or less, are further evaluated for the ability to stimulate HTL responses.

Conventional assays utilized to detect T cell responses include proliferation assays, lymphokine secretion assays, direct cytotoxicity assays, and limiting dilution assays. For example, antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells. Alternatively, mutant non-human mammalian cell lines that are deficient in their ability to load class I molecules with internally processed peptides and that have been transfected with the appropriate human class I gene, may be used to test for the capacity of the peptide to induce *in vitro* primary CTL responses.

Peripheral blood mononuclear cells (PBMCs) may be used as the responder cell source of CTL precursors. The appropriate antigen-presenting cells are incubated with peptide, after which the peptide-loaded antigen-presenting cells are then incubated with the responder cell population under optimized culture conditions. Positive CTL activation can be determined by assaying the culture for the presence of CTLs that kill radio-labeled target cells, both specific peptide-pulsed targets as well as target cells expressing endogenously processed forms of the antigen from which the peptide sequence was derived.

Additionally, a method has been devised which allows direct quantification of antigen-specific T cells by staining with Fluorescein-labelled HLA tetrameric complexes (Altman, J. D. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:10330, 1993; Altman, J. D. *et al.*, *Science* 274:94, 1996). Other relatively recent technical developments include staining for intracellular lymphokines, and interferon-γ release assays or ELISPOT assays. Tetramer staining, intracellular lymphokine staining and ELISPOT assays all appear to be at least 10-fold more sensitive than more conventional assays (Lalvani, A. *et al.*, *J. Exp. Med.* 186:859, 1997; Dunbar, P. R. *et al.*, *Curr. Biol.* 8:413, 1998; Murali-Krishna, K. *et al.*, *Immunity* 8:177, 1998).

HTL activation may also be assessed using such techniques known to those in the art such as T cell proliferation and secretion of lymphokines, *e.g.* IL-2 (*see, e.g.* Alexander *et al.*, Immunity 1:751-761, 1994).

Alternatively, immunization of HLA transgenic mice can be used to determine immunogenicity of peptide epitopes. Several transgenic mouse models including mice with human A2.1, A11 (which can additionally be used to analyze HLA-A3 epitopes), and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed. Additional transgenic mouse models with other HLA alleles may be generated as necessary. The mice may be immunized with peptides emulsified in Incomplete Freund's Adjuvant and the resulting T cells tested for their capacity to recognize peptide-pulsed target cells and target cells transfected with appropriate genes. CTL responses may be analyzed using cytotoxicity assays described above. Similarly, HTL responses may be analyzed using such assays as T cell proliferation or secretion of lymphokines.

IV.J. Use of Peptide Epitopes as Diagnostic Agents and for Evaluating Immune Responses

In one embodiment of the invention, HLA class I and class II binding peptides as described herein are used as reagents to evaluate an immune response. The immune response to be evaluated is induced by using as an immunogen any agent that may result in the production of antigen-specific CTLs or HTLs that recognize and bind to the peptide epitope(s) to be employed as the reagent. The peptide reagent need not be used as the immunogen. Assay systems that are used for such an analysis include relatively recent technical developments such as tetramers, staining for intracellular lymphokines and interferon release assays, or ELISPOT assays.

For example, peptides of the invention are used in tetramer staining assays to assess peripheral blood mononuclear cells for the presence of antigen-specific CTLs following exposure to a tumor cell antigen or an immunogen. The HLA-tetrameric complex is used to directly visualize antigen-specific CTLs (*see, e.g.*, Ogg *et al.*, *Science* 279:2103-2106, 1998; and Altman *et al.*, *Science* 174:94-96, 1996) and determine the frequency of the antigen-specific CTL population in a sample of peripheral blood mononuclear cells. A tetramer reagent using a peptide of the invention is generated as follows: A peptide that binds to an HLA molecule is refolded in the presence of the

corresponding HLA heavy chain and β_2-microglobulin to generate a trimolecular complex. The complex is biotinylated at the carboxyl terminal end of the heavy chain at a site that was previously engineered into the protein. Tetramer formation is then induced by the addition of streptavidin. By means of fluorescently labeled streptavidin, the tetramer can be used to stain antigen-specific cells. The cells can then be identified, for example, by flow cytometry. Such an analysis may be used for diagnostic or prognostic purposes. Cells identified by the procedure can also be used for therapeutic purposes.

Peptides of the invention are also used as reagents to evaluate immune recall responses (*see, e.g.*, Bertoni *et al.*, *J. Clin. Invest.* 100:503-513, 1997 and Penna *et al.*, *J. Exp. Med.* 174:1565-1570, 1991). For example, patient PBMC samples from individuals with cancer are analyzed for the presence of antigen-specific CTLs or HTLs using specific peptides. A blood sample containing mononuclear cells can be evaluated by cultivating the PBMCs and stimulating the cells with a peptide of the invention. After an appropriate cultivation period, the expanded cell population can be analyzed, for example, for CTL or for HTL activity.

The peptides are also used as reagents to evaluate the efficacy of a vaccine. PBMCs obtained from a patient vaccinated with an immunogen are analyzed using, for example, either of the methods described above. The patient is HLA typed, and peptide epitope reagents that recognize the allele-specific molecules present in that patient are selected for the analysis. The immunogenicity of the vaccine is indicated by the presence of epitope-specific CTLs and/or HTLs in the PBMC sample.

The peptides of the invention are also used to make antibodies, using techniques well known in the art (see, *e.g.* *CURRENT PROTOCOLS IN IMMUNOLOGY*, Wiley/Greene, NY; and *Antibodies A Laboratory Manual,* Harlow and Lane, Cold Spring Harbor Laboratory Press, 1989), which may be useful as reagents to diagnose or monitor cancer. Such antibodies include those that recognize a peptide in the context of an HLA molecule, *i.e.*, antibodies that bind to a peptide-MHC complex.

IV.K. Vaccine Compositions

Vaccines and methods of preparing vaccines that contain an immunogenically effective amount of one or more peptides as described herein are further embodiments of the invention. Once appropriately immunogenic epitopes have been defined, they can be sorted and delivered by various means, herein referred to as

"vaccine" compositions. Such vaccine compositions can include, for example, lipopeptides (*e.g.*,Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991: Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995), peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g.*, Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998), multiple antigen peptide systems (MAPs) (*see e.g.*, Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990), particles of viral or synthetic origin (*e.g.*, Kofler, N. *et al.*, *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995), adjuvants (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993), liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996), or, naked or particle absorbed cDNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccines of the invention include nucleic acid-mediated modalities. DNA or RNA encoding one or more of the peptides of the invention can also be administered to a patient. This approach is described, for instance, in Wolff *et. al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can also be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. As an example of this approach, vaccinia virus is used as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into a host bearing a tumor, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits a host CTL and/or HTL response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein.

Furthermore, vaccines in accordance with the invention encompass compositions of one or more of the claimed peptides. A peptide can be present in a vaccine individually. Alternatively, the peptide can exist as a homopolymer comprising multiple copies of the same peptide, or as a heteropolymer of various peptides. Polymers have the advantage of increased immunological reaction and, where different peptide epitopes are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the pathogenic organism or tumor-related peptide targeted for an immune response. The composition can be a naturally occurring region of an antigen or can be prepared, *e.g.*, recombinantly or by chemical synthesis.

Carriers that can be used with vaccines of the invention are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza, hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable (*i.e.*, acceptable) diluent such as water, or saline, preferably phosphate buffered saline. The vaccines also typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glycerylcysteinlyseryl- serine (P_3CSS).

Upon immunization with a peptide composition in accordance with the invention, via injection, aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by producing large amounts of CTLs and/or HTLs specific for the desired antigen. Consequently, the host becomes at least partially immune to later infection, or at least partially resistant to developing an ongoing chronic infection, or derives at least some therapeutic benefit when the antigen was tumor-associated.

In some embodiments, it may be desirable to combine the class I peptide components with components that induce or facilitate neutralizing antibody and or helper T cell responses to the target antigen of interest. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. An alternative embodiment of such a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PADRE™ (Epimmune, San Diego, CA) molecule (described, for example, in U.S. Patent Number 5,736,142).

A vaccine of the invention can also include antigen-presenting cells (APC), such as dendritic cells (DC), as a vehicle to present peptides of the invention. Vaccine compositions can be created *in vitro*, following dendritic cell mobilization and harvesting, whereby loading of dendritic cells occurs *in vitro*. For example, dendritic cells are transfected, *e.g.*, with a minigene in accordance with the invention, or are pulsed with peptides. The dendritic cell can then be administered to a patient to elicit immune responses *in vivo*.

Vaccine compositions, either DNA- or peptide-based, can also be administered *in vivo* in combination with dendritic cell mobilization whereby loading of dendritic cells occurs *in vivo*.

Antigenic peptides are used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTL or HTL cells, can be used to treat tumors in patients that do not respond to other conventional forms of therapy, or will not respond to a therapeutic vaccine peptide or nucleic acid in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular tumor-associated antigen are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of antigen-presenting cells, such as dendritic cells, and the appropriate immunogenic peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are

infused back into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cell (an infected cell or a tumor cell). Transfected dendritic cells may also be used as antigen presenting cells.

The vaccine compositions of the invention can also be used in combination with other treatments used for cancer, including use in combination with immune adjuvants such as IL-2, IL-12, GM-CSF, and the like.

Preferably, the following principles are utilized when selecting an array of epitopes for inclusion in a polyepitopic composition for use in a vaccine, or for selecting discrete epitopes to be included in a vaccine and/or to be encoded by nucleic acids such as a minigene. It is preferred that each of the following principles are balanced in order to make the selection. The multiple epitopes to be incorporated in a given vaccine composition may be, but need not be, contiguous in sequence in the native antigen from which the epitopes are derived.

1.) Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with tumor clearance. For HLA Class I this includes 3-4 epitopes that come from at least one TAA. For HLA Class II a similar rationale is employed; again 3-4 epitopes are selected from at least one TAA (*see e.g.*, Rosenberg *et al.*, *Science* 278:1447-1450). Epitopes from one TAA may be used in combination with epitopes from one or more additional TAAs to produce a vaccine that targets tumors with varying expression patterns of frequently-expressed TAAs as described, *e.g.*, in Example 15.

2.) Epitopes are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC_{50} of 500 nM or less, often 200 nM or less; and for Class II an IC_{50} of 1000 nM or less.

3.) Sufficient supermotif bearing-peptides, or a sufficient array of allele-specific motif-bearing peptides, are selected to give broad population coverage. For example, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth, or redundancy of, population coverage.

4.) When selecting epitopes from cancer-related antigens it is often useful to select analogs because the patient may have developed tolerance to the native epitope. When selecting epitopes for infectious disease-related antigens it is preferable to select either native or analoged epitopes.

5.) Of particular relevance are epitopes referred to as "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. A nested peptide sequence can comprise both HLA class I and HLA class II epitopes. When providing nested epitopes, a general objective is to provide the greatest number of epitopes per sequence. Thus, an aspect is to avoid providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a multi-epitopic sequence, such as a sequence comprising nested epitopes, it is generally important to screen the sequence in order to insure that it does not have pathological or other deleterious biological properties.

6.) If a polyepitopic protein is created, or when creating a minigene, an objective is to generate the smallest peptide that encompasses the epitopes of interest. This principle is similar, if not the same as that employed when selecting a peptide comprising nested epitopes. However, with an artificial polyepitopic peptide, the size minimization objective is balanced against the need to integrate any spacer sequences between epitopes in the polyepitopic protein. Spacer amino acid residues can, for example, be introduced to avoid junctional epitopes (an epitope recognized by the immune system, not present in the target antigen, and only created by the man-made juxtaposition of epitopes), or to facilitate cleavage between epitopes and thereby enhance epitope presentation. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

IV.K.1. Minigene Vaccines

A number of different approaches are available which allow simultaneous delivery of multiple epitopes. Nucleic acids encoding the peptides of the invention are a particularly useful embodiment of the invention. Epitopes for inclusion in a minigene are preferably selected according to the guidelines set forth in the previous section. A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding a peptide comprising one or multiple epitopes of the invention.

The use of multi-epitope minigenes is described below and in, *e.g.*, co-pending application U.S.S.N. 09/311,784; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822, 1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998. For example, a multi-epitope DNA plasmid encoding supermotif- and/or motif-bearing PSA, PSM, PAP, and hK2 epitopes derived from multiple regions of one or more of the prostate cancer-associated antigens, the PADRE™ universal helper T cell epitope (or multiple HTL epitopes from PSA, PSM, PAP, and hK2), and an endoplasmic reticulum-translocating signal sequence can be engineered. A vaccine may also comprise epitopes that are derived from other TAAs.

The immunogenicity of a multi-epitopic minigene can be tested in transgenic mice to evaluate the magnitude of CTL induction responses against the epitopes tested. Further, the immunogenicity of DNA-encoded epitopes *in vivo* can be correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA plasmid. Thus, these experiments can show that the minigene serves to both: 1.) generate a CTL response and 2.) that the induced CTLs recognized cells expressing the encoded epitopes.

For example, to create a DNA sequence encoding the selected epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes may be reverse translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that when translated, a continuous polypeptide sequence is created. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequences that can be reverse translated and included in the minigene sequence include: HLA class I epitopes, HLA class II epitopes, a ubiquitination signal sequence, and/or an endoplasmic reticulum targeting signal. In addition, HLA presentation of CTL and HTL epitopes may be improved by including synthetic (*e.g.* poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger peptides comprising the epitope(s) are within the scope of the invention.

The minigene sequence may be converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) may be synthesized, phosphorylated, purified and

annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope polypeptide, can then be cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the target cells. Several vector elements are desirable: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing minigene expression.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence, if desired to enhance immunogenicity.

In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (included to enhance or decrease immunogenicity) can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (*e.g.*, IL-2, IL-12, GM-CSF), cytokine-inducing molecules (*e.g.*, LeIF), costimulatory

molecules, or for HTL responses, pan-DR binding proteins (PADRE™, Epimmune, San Diego, CA). Helper (HTL) epitopes can be joined to intracellular targeting signals and expressed separately from expressed CTL epitopes; this allows direction of the HTL epitopes to a cell compartment different than that of the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the HLA class II pathway, thereby improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (*e.g.* TGF-β) may be beneficial in certain diseases.

Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffered saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of minigene DNA vaccines, an alternative method for formulating purified plasmid DNA may be desirable. A variety of methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, *e.g.*, as described by WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Pat No. 5,279,833; WO 91/06309; and Felgner, *et al., Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and HLA class I presentation of minigene-encoded CTL epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent

on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 (^{51}Cr) labeled and used as target cells for epitope-specific CTL lines; cytolysis, detected by ^{51}Cr release, indicates both production of, and HLA presentation of, minigene-encoded CTL epitopes. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (*e.g.,* IM for DNA in PBS, intraperitoneal (IP) for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTL effector cells, assays are conducted for cytolysis of peptide-loaded, ^{51}Cr-labeled target cells using standard techniques. Lysis of target cells that were sensitized by HLA loaded with peptide epitopes, corresponding to minigene-encoded epitopes, demonstrates DNA vaccine function for *in vivo* induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.

Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of DNA are administered. In a further alternative embodiment, DNA can be adhered to particles, such as gold particles.

Minigenes can also be delivered using other bacterial or viral delivery systems well known in the art, *e.g.*, an expression construct encoding epitopes of the invention can be incorporated into a viral vector such as vaccinia.

IV.K.2. Combinations of CTL Peptides with Helper Peptides

Vaccine compositions comprising the peptides of the present invention can be modified to provide desired attributes, such as improved serum half-life, or to enhance immunogenicity.

For instance, the ability of a peptide to induce CTL activity can be enhanced by linking the peptide to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. The use of T helper epitopes in conjunction

with CTL epitopes to enhance immunogenicity is illustrated, for example, in the co-pending applications U.S.S.N. 08/820,360, U.S.S.N. 08/197,484, and U.S.S.N. 08/464,234.

Although a CTL peptide can be directly linked to a T helper peptide, often CTL epitope/HTL epitope conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues and sometimes 10 or more residues. The CTL peptide epitope can be linked to the T helper peptide epitope either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the T helper peptide may be acylated.

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in the majority of the population. This can be accomplished by selecting amino acid sequences that bind to many, most, or all of the HLA class II molecules. These are known as "loosely HLA-restricted" or "promiscuous" T helper sequences. Examples of peptides that are promiscuous include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS), and *Streptococcus* 18kD protein at positions 116 (GAVDSILGGVATYGAA). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferrably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAWTLKAAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and "a" is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles,

~~and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.~~

HTL peptide epitopes can also be modified to alter their biological properties. For example, they can be modified to include D-amino acids to increase their resistance to proteases and thus extend their serum half life, or they can be conjugated to other molecules such as lipids, proteins, carbohydrates, and the like to increase their biological activity. For example, the T helper peptide can be conjugated to one or more palmitic acid chains at either the amino or carboxyl termini.

IV.K.3. Combinations of CTL Peptides with T Cell Priming Agents

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes cytotoxic T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. For example, palmitic acid residues can be attached to the ε-and α-amino groups of a lysine residue and then linked, *e.g.*, via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant. A preferred immunogenic composition comprises palmitic acid attached to ε- and α- amino groups of Lys, which is attached via linkage, *e.g.*, Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinlyseryl- serine (P_3CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide (*see*, *e.g.*, Deres, *et al.*, *Nature* 342:561, 1989). Peptides of the invention can be coupled to P_3CSS, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P_3CSS-conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses.

CTL and/or HTL peptides can also be modified by the addition of amino acids to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support or larger peptide, for modifying the physical or chemical

properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or the like, can be introduced at the C- or N-terminus of the peptide or oligopeptide, particularly class I peptides. However, it is to be noted that modification at the carboxyl terminus of a CTL epitope may, in some cases, alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH_2 acylation, *e.g.*, by alkanoyl (C_1-C_{20}) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule.

IV.K.4. Vaccine Compositions Comprising DC Pulsed with CTL and/or HTL Peptides

An embodiment of a vaccine composition in accordance with the invention comprises *ex vivo* administration of a cocktail of epitope-bearing peptides to PBMC, or isolated DC therefrom, from the patient's blood. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides. In this embodiment, a vaccine comprises peptide-pulsed DCs which present the pulsed peptide epitopes complexed with HLA molecules on their surfaces.

The DC can be pulsed *ex vivo* with a cocktail of peptides, some of which stimulate CTL response to one or more antigens of interest, *e.g.*, prostate-associated antigens such as PSA, PSM, PAP, kallikrein, and the like. Optionally, a helper T cell peptide such as a PADRE™ family molecule can be included to facilitate the CTL response.

IV.L. Administration of Vaccines for Therapeutic or Prophylactic Purposes

The peptides of the present invention and pharmaceutical and vaccine compositions of the invention are typically used therapeutically to treat cancer, particularly prostate cancer. Vaccine compositions containing the peptides of the invention are typically administered to a prostate cancer patient who has a malignancy associated with expression of one or more prostate-associated antigens. Alternatively,

vaccine compositions can be administered to an individual susceptible to, or otherwise at risk for developing prostate cancer.

In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective CTL and/or HTL response to the tumor antigen and to cure or at least partially arrest or slow symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, *e.g.*, the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician.

As noted above, peptides comprising CTL and/or HTL epitopes of the invention induce immune responses when presented by HLA molecules and contacted with a CTL or HTL specific for an epitope comprised by the peptide. The peptides (or DNA encoding them) can be administered individually or as fusions of one or more peptide sequences. The manner in which the peptide is contacted with the CTL or HTL is not critical to the invention. For instance, the peptide can be contacted with the CTL or HTL either *in vivo* or *in vitro*. If the contacting occurs *in vivo*, the peptide itself can be administered to the patient, or other vehicles, *e.g.*, DNA vectors encoding one or more peptides, viral vectors encoding the peptide(s), liposomes and the like, can be used, as described herein.

When the peptide is contacted *in vitro*, the vaccinating agent can comprise a population of cells, *e.g.*, peptide-pulsed dendritic cells, or TAA-specific CTLs, which have been induced by pulsing antigen-presenting cells *in vitro* with the peptide or by transfecting antigen-presenting cells with a minigene of the invention. Such a cell population is subsequently administered to a patient in a therapeutically effective dose.

For therapeutic use, administration should generally begin at the first diagnosis of cancer. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. The embodiment of the vaccine composition (*i.e.*, including, but not limited to embodiments such as peptide cocktails, polyepitopic polypeptides, minigenes, or TAA-specific CTLs or pulsed dendritic cells) delivered to the patient may vary according to the stage of the disease or the patient's health status. For example, a vaccine comprising TAA-specific CTLs may be more efficacious in killing tumor cells in patients with advanced disease than alternative embodiments.

The vaccine compositions of the invention may also be used therapeutically in combination with treatments such as surgery. An example is a situation in which a patient has undergone surgery to remove a primary tumor and the vaccine is then used to slow or prevent recurrence and/or metastasis.

Where susceptible individuals, *e.g.*, individuals who may be diagnosed as being genetically pre-disposed to developing a prostate tumor, are identified prior to diagnosis of cancer, the composition can be targeted to them, thus minimizing the need for administration to a larger population.

The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg. Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. Initial doses followed by boosting doses at established intervals, *e.g.,* from four weeks to six months, may be required, possibly for a prolonged period of time to effectively treat a patient. Boosting dosages of between about 1.0 μg to about 50,000 μg of peptide pursuant to a boosting regimen over weeks to months may be administered depending upon the patient's response and condition as determined by measuring the specific activity of CTL and HTL obtained from the patient's blood.

Administration should continue until at least clinical symptoms or laboratory tests indicate that the tumor has been eliminated or that the tumor cell burden has been substantially reduced and for a period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

In certain embodiments, peptides and compositions of the present invention are employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides in preferred compositions of the invention, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

The vaccine compositions of the invention can also be used as prophylactic agents. For example, the compositions can be administered to individuals at risk of developing prostate cancer. Generally the dosage for an initial prophylactic

immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg. Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 μg to about 50,000 μg of peptide administered at defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine may be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's blood.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, intrathecal, or local administration. Preferably, the pharmaceutical compositions are administered parentally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, *etc.*

The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, *i.e.*, from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, *etc.*, in accordance with the particular mode of administration selected.

A human unit dose form of the peptide composition is typically included in a pharmaceutical composition that comprises a human unit dose of an acceptable carrier, preferably an aqueous carrier, and is administered in a volume of fluid that is known by those of skill in the art to be used for administration of such compositions to humans (*see*,

e.g., Remington's Pharmaceutical Sciences, 17th Edition, A. Gennaro, Editor, Mack Publishing Co., Easton, Pennsylvania, 1985).

The peptides of the invention may also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or to target selectively to infected cells, as well as to increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to a receptor prevalent among lymphoid cells, such as monoclonal antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka, *et al., Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

For targeting cells of the immune system, a ligand to be incorporated into the liposome can include, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical

percentages of peptides are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, *e.g.*, lecithin for intranasal delivery.

IV.M. Kits

The peptide and nucleic acid compositions of this invention can be provided in kit form together with instructions for vaccine administration. Typically the kit would include desired peptide compositions in a container, preferably in unit dosage form and instructions for administration. An alternative kit would include a minigene construct with desired nucleic acids of the invention in a container, preferably in unit dosage form together with instructions for administration. Lymphokines such as IL-2 or IL-12 may also be included in the kit. Other kit components that may also be desirable include, for example, a sterile syringe, booster dosages, and other desired excipients.

Epitopes in accordance with the present invention were successfully used to induce an immune response. Immune responses with these epitopes have been induced by administering the epitopes in various forms. The epitopes have been administered as peptides, as nucleic acids, and as viral vectors comprising nucleic acids that encode the epitope(s) of the invention. Upon administration of peptide-based epitope forms, immune responses have been induced by direct loading of an epitope onto an empty HLA molecule that is expressed on a cell, and via internalization of the epitope and processing via the HLA class I pathway; in either event, the HLA molecule expressing the epitope was then able to interact with and induce a CTL response. Peptides can be delivered directly or using such agents as liposomes. They can additionally be delivered using ballistic delivery, in which the peptides are typically in a crystalline form. When DNA is used to induce an immune response, it is administered either as naked DNA, generally in a dose range of approximately 1-5mg, or via the ballistic "gene gun" delivery, typically in

a dose range of approximately 10-100 μg. The DNA can be delivered in a variety of conformations, *e.g.*, linear, circular *etc.* Various viral vectors have also successfully been used that comprise nucleic acids which encode epitopes in accordance with the invention.

Accordingly compositions in accordance with the invention exist in several forms. Embodiments of each of these composition forms in accordance with the invention have been successfully used to induce an immune response.

One composition in accordance with the invention comprises a plurality of peptides. This plurality or cocktail of peptides is generally admixed with one or more pharmaceutically acceptable excipients. The peptide cocktail can comprise multiple copies of the same peptide or can comprise a mixture of peptides. The peptides can be analogs of naturally occurring epitopes. The peptides can comprise artificial amino acids and/or chemical modifications such as addition of a surface active molecule, *e.g.*, lipidation; acetylation, glycosylation, biotinylation, phosphorylation etc. The peptides can be CTL or HTL epitopes. In a preferred embodiment the peptide cocktail comprises a plurality of different CTL epitopes and at least one HTL epitope. The HTL epitope can be naturally or non-naturally (e.g., PADRE®, Epimmune Inc., San Diego, CA). The number of distinct epitopes in an embodiment of the invention is generally a whole unit integer from one through one hundred fifty (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or, 100).

An additional embodiment of a composition in accordance with the invention comprises a polypeptide multi-epitope construct, *i.e.*, a polyepitopic peptide. Polyepitopic peptides in accordance with the invention are prepared by use of technologies well-known in the art. By use of these known technologies, epitopes in accordance with the invention are connected one to another. The polyepitopic peptides can be linear or non-linear, *e.g.*, multivalent. These polyepitopic constructs can comprise artificial amino acids, spacing or spacer amino acids, flanking amino acids, or chemical modifications between adjacent epitope units. The polyepitopic construct can be a heteropolymer or a homopolymer. The polyepitopic constructs generally comprise epitopes in a quantity of any whole unit integer between 2-150 (*e.g.*, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33,

34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or, 100). The polyepitopic construct can comprise CTL and/or HTL epitopes. One or more of the epitopes in the construct can be modified, *e.g.*, by addition of a surface active material, *e.g.* a lipid, or chemically modified, *e.g.*, acetylation, *etc.* Moreover, bonds in the multiepitopic construct can be other than peptide bonds, *e.g.*, covalent bonds, ester or ether bonds, disulfide bonds, hydrogen bonds, ionic bonds *etc.*

Alternatively, a composition in accordance with the invention comprises construct which comprises a series, sequence, stretch, *etc.*, of amino acids that have homology to (*i.e.*, corresponds to or is contiguous with) to a native sequence. This stretch of amino acids comprises at least one subsequence of amino acids that, if cleaved or isolated from the longer series of amino acids, functions as an HLA class I or HLA class II epitope in accordance with the invention. In this embodiment, the peptide sequence is modified, so as to become a construct as defined herein, by use of any number of techniques known or to be provided in the art. The polyepitopic constructs can contain homology to a native sequence in any whole unit integer increment from 70-100%, e.g., 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or, 100 percent.

A further embodiment of a composition in accordance with the invention is an antigen presenting cell that comprises one or more epitopes in accordance with the invention. The antigen presenting cell can be a "professional" antigen presenting cell, such as a dendritic cell. The antigen presenting cell can comprise the epitope of the invention by any means known or to be determined in the art. Such means include pulsing of dendritic cells with one or more individual epitopes or with one or more peptides that comprise multiple epitopes, by nucleic acid administration such as ballistic nucleic acid delivery or by other techniques in the art for administration of nucleic acids, including vector-based, *e.g.* viral vector, delivery of nucleic acids.

Further embodiments of compositions in accordance with the invention comprise nucleic acids that encode one or more peptides of the invention, or nucleic acids which encode a polyepitopic peptide in accordance with the invention. As appreciated by one of ordinary skill in the art, various nucleic acids compositions will encode the same peptide due to the redundancy of the genetic code. Each of these nucleic acid compositions falls within the scope of the present invention. This embodiment of the

invention comprises DNA or RNA, and in certain embodiments a combination of DNA and RNA. It is to be appreciated that any composition comprising nucleic acids that will encode a peptide in accordance with the invention or any other peptide based composition in accordance with the invention, falls within the scope of this invention.

It is to be appreciated that peptide-based forms of the invention (as well as the nucleic acids that encode them) can comprise analogs of epitopes of the invention generated using priniciples already known, or to be known, in the art. Principles related to analoging are now known in the art, and are disclosed herein; moreover, analoging principles (heteroclitic analoging) are disclosed in co-pending application serial number U.S.S.N. 09/226,775 filed 6 January 1999. Generally the compositions of the invention are isolated or purified.

The invention will be described in greater detail by way of specific examples. The following examples are offered for illustrative purposes, and are not intended to limit the invention in any manner. Those of skill in the art will readily recognize a variety of non-critical parameters that can be changed or modified to yield alternative embodiments in accordance with the invention.

V. EXAMPLES

The following examples illustrate identification, selection, and use of immunogenic Class I and Class II peptide epitopes for inclusion in vaccine compositions.

Example 1. HLA Class I and Class II Binding Assays

The following example of peptide binding to HLA molecules demonstrates quantification of binding affinities of HLA class I and class II peptides. Binding assays can be performed with peptides that are either motif-bearing or not motif-bearing.

Cell lysates were prepared and HLA molecules purified in accordance with disclosed protocols (Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al., J. Immunol.* 154:247 (1995); Sette, *et al., Mol. Immunol.* 31:813 (1994)). cells/ml in 50 mM Tris. The cell lines used as sources of HLA molecules and the antibodies used for the extraction of the HLA molecules from the cell lysates are also described in these publications.

Epstein-Barr virus (EBV)-transformed homozygous cell lines, fibroblasts, CIR, or 721.221-transfectants were used as sources of HLA class I molecules. These

cells were maintained *in vitro* by culture in RPMI 1640 medium supplemented with 2mM L-glutamine (GIBCO, Grand Island, NY), 50μM 2-ME, 100μg/ml of streptomycin, 100U/ml of penicillin (Irvine Scientific) and 10% heat-inactivated FCS (Irvine Scientific, Santa Ana, CA). Cells were grown in 225-cm^2 tissue culture flasks or, for large-scale cultures, in roller bottle apparatuses.

Cell lysates were prepared and HLA molecules purified in accordance with disclosed protocols (Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al., J. Immunol.* 154:247 (1995); Sette, *et al., Mol. Immunol.* 31:813 (1994)). Briefly, cells were lysed at a concentration of 10^8 cells/ml in 50 mM Tris-HCl, pH 8.5, containing 1% Nonidet P-40 (Fluka Biochemika, Buchs, Switzerland), 150 mM NaCl, 5 mM EDTA, and 2 mM PMSF. Lysates were cleared of debris and nuclei by centrifugation at 15,000 x g for 30min.

HLA molecules were purified from lysates by affinity chromatography. Lysates prepared as above were passed twice through two pre-columns of inactivated Sepharose CL4-B and protein A-Sepharose. Next, the lysate was passed over a column of Sepharose CL-4B beads coupled to an appropriate antibody. The anti-HLA column was then washed with 10-column volumes of 10mM Tris-HCL, pH 8.0, in 1% NP-40, PBS, 2-column volumes of PBS, and 2-column volumes of PBS containing 0.4% n-octylglucoside. Finally, MHC molecules were eluted with 50mM diethylamine in 0.15M NaCl containing 0.4% n-octylglucoside, pH 11.5. A 1/25 volume of 2.0M Tris, pH 6.8, was added to the eluate to reduce the pH to ~8.0. Eluates were then concentrated by centrifugation in Centriprep 30 concentrators at 2000 rpm (Amicon, Beverly, MA). Protein content was evaluated by a BCA protein assay (Pierce Chemical Co., Rockford, IL) and confirmed by SDS-PAGE.

A detailed description of the protocol utilized to measure the binding of peptides to Class I and Class II MHC has been published (Sette *et al.*, *Mol. Immunol.* 31:813, 1994; Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998). Briefly, purified MHC molecules (5 to 500nM) were incubated with various unlabeled peptide inhibitors and 1-10nM ^{125}I-radiolabeled probe peptides for 48h in PBS containing 0.05% Nonidet P-40 (NP40) (or 20% w/v digitonin for H-2 IA assays) in the presence of a protease inhibitor cocktail. The final concentrations of protease inhibitors (each from CalBioChem, La Jolla, CA) were 1 mM PMSF, 1.3 nM 1.10 phenanthroline, 73 μM pepstatin A, 8mM EDTA, 6mM

N-ethylmaleimide (for Class II assays), and 200 μM N alpha-p-tosyl-L-lysine chloromethyl ketone (TLCK). All assays were performed at pH 7.0 with the exception of DRB1*0301, which was performed at pH 4.5, and DRB1*1601 (DR2w21β_1) and DRB4*0101 (DRw53), which were performed at pH 5.0. pH was adjusted as described elsewhere (*see* Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998).

Following incubation, MHC-peptide complexes were separated from free peptide by gel filtration on 7.8 mm x 15 cm TSK200 columns (TosoHaas 16215, Montgomeryville, PA), eluted at 1.2 mls/min with PBS pH 6.5 containing 0.5% NP40 and 0.1% NaN_3. Because the large size of the radiolabeled peptide used for the DRB1*1501 (DR2w2β_1) assay makes separation of bound from unbound peaks more difficult under these conditions, all DRB1*1501 (DR2w2β_1) assays were performed using a 7.8mm x 30cm TSK2000 column eluted at 0.6 mls/min. The eluate from the TSK columns was passed through a Beckman 170 radioisotope detector, and radioactivity was plotted and integrated using a Hewlett-Packard 3396A integrator, and the fraction of peptide bound was determined.

Radiolabeled peptides were iodinated using the chloramine-T method. Representative radiolabeled probe peptides utilized in each assay, and its assay specific IC_{50} nM, are summarized in Tables IV and V. Typically, in preliminary experiments, each MHC preparation was titered in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of the total radioactivity. All subsequent inhibition and direct binding assays were performed using these HLA concentrations.

Since under these conditions [label]<[HLA] and $IC_{50} \geq$[HLA], the measured IC_{50} values are reasonable approximations of the true K_D values. Peptide inhibitors are typically tested at concentrations ranging from 120 μg/ml to 1.2 ng/ml, and are tested in two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide by dividing the IC_{50} of a positive control for inhibition by the IC_{50} for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For inter-experiment comparisons, relative binding values are compiled. These values can subsequently be converted back into IC_{50} nM values by dividing the IC_{50} nM of the positive controls for inhibition by the relative binding of the peptide of interest. This

method of data compilation has proven to be the most accurate and consistent for comparing peptides that have been tested on different days, or with different lots of purified MHC.

Because the antibody used for HLA-DR purification (LB3.1) is α-chain specific, β_1 molecules are not separated from β_3 (and/or β_4 and β_5) molecules. The β_1 specificity of the binding assay is obvious in the cases of DRB1*0101 (DR1), DRB1*0802 (DR8w2), and DRB1*0803 (DR8w3), where no β_3 is expressed. It has also been demonstrated for DRB1*0301 (DR3) and DRB3*0101 (DR52a), DRB1*0401 (DR4w4), DRB1*0404 (DR4w14), DRB1*0405 (DR4w15), DRB1*1101 (DR5), DRB1*1201 (DR5w12), DRB1*1302 (DR6w19) and DRB1*0701 (DR7). The problem of β chain specificity for DRB1*1501 (DR2w2β_1), DRB5*0101 (DR2w2β_2), DRB1*1601 (DR2w21β_1), DRB5*0201 (DR51Dw21), and DRB4*0101 (DRw53) assays is circumvented by the use of fibroblasts. Development and validation of assays with regard to DRβ molecule specificity have been described previously (*see, e.g.*, Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998).

Binding assays as outlined above may be used to analyze supermotif and/or motif-bearing epitopes as, for example, described in Example 2.

Example 2. Identification of HLA Supermotif- and Motif-Bearing CTL Candidate Epitopes

Vaccine compositions of the invention may include multiple epitopes that comprise multiple HLA supermotifs or motifs to achieve broad population coverage. This example illustrates the identification of supermotif- and motif-bearing epitopes for the inclusion in such a vaccine composition. Calculation of population coverage is performed using the strategy described below.

Computer searches and algorthims for identification of supermotif and/or motif-bearing epitopes

The searches performed to identify the motif-bearing peptide sequences in Examples 2 and 5 employ protein sequence data for prostate cancer-associated antigens.

Computer searches for epitopes bearing HLA Class I or Class II supermotifs or motifs were performed as follows. All translated protein sequences were analyzed using a text string search software program, *e.g.*, MotifSearch 1.4 (D. Brown,

San Diego) to identify potential peptide sequences containing appropriate HLA binding motifs; alternative programs are readily produced in accordance with information in the art in view of the motif/supermotif disclosure herein. Furthermore, such calculations can be made mentally.

Identified A2-, A3-, and DR-supermotif sequences were scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II molecules. These polynomial algorithms take into account both extended and refined motifs (that is, to account for the impact of different amino acids at different positions), and are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$\text{“}\Delta G\text{”} = a_{1i} \times a_{2i} \times a_{3i} \ldots\ldots \times a_{ni}$$

where a_{ji} is a coefficient which represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (i.e., independent binding of individual side-chains). When residue j occurs at position i in the peptide, it is assumed to contribute a constant amount j_i to the free energy of binding of the peptide irrespective of the sequence of the rest of the peptide. This assumption is justified by studies from our laboratories that demonstrated that peptides are bound to MHC and recognized by T cells in essentially an extended conformation (data omitted herein).

The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (*see* also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all i positions, anchor and non-anchor alike, the geometric mean of the average relative binding (ARB) of all peptides carrying j is calculated relative to the remainder of the group, and used as the estimate of j_i. For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

Selection of HLA-A2 supertype cross-reactive peptides

The complete protein sequences of the prostate cancer-associated antigens PAP, PSA, PSM, and hK2 were obtained from GenBank and scanned, utilizing motif identification software, to identify 8-, 9-, 10-, and 11-mer sequences containing the HLA-A2-supermotif main anchor specificity.

HLA-A2 supermotif-bearing sequences are shown in Table VII. These sequences are then scored using the A2 algorithm and the peptides corresponding to the positive-scoring sequences are synthesized and tested for their capacity to bind purified HLA-A*0201 molecules *in vitro* (HLA-A*0201 is considered a prototype A2 supertype molecule).

Examples of peptides that were identified that bind to HLA-A*0201 with IC_{50} values ≤500 nM are shown in Tables XXII and XXIII. These peptides were then tested for the capacity to bind to additional A2-supertype molecules (A*0202, A*0203, A*0206, and A*6802). Peptides that bind to at least three of the five A2-supertype alleles tested are deemed A2-supertype cross-reactive binders. Preferred peptides bind at an affinity equal to or less than 500 nM to three or more HLA-A2 supertype molecules. Examples of such peptides are set out in Table XXIII. (Due to the homology described above, a number of CTL and HTL epitopes are represented in both the PSA and hK2 antigens. This is represented in Tables XXIII and XXIV by the headings source and alternate source.)

Selection of HLA-A3 supermotif-bearing epitopes

The protein sequences scanned above were also examined for the presence of peptides with the HLA-A3-supermotif primary anchors using methodology similar to that performed to identify HLA-A2 supermotif-bearing epitopes.

Peptides corresponding to the supermotif-bearing sequences are then synthesized and tested for binding to HLA-A*0301 and HLA-A*1101 molecules, the two most prevalent A3-supertype alleles. The peptides that are found to bind one of the two alleles with binding affinities of ≤500 nM, preferably ≤ 200 nM, are then tested for binding cross-reactivity to the other common A3-supertype alleles (A*3101, A*3301, and A*6801) to identify those that can bind at least three of the five HLA-A3-supertype molecules tested.

Selection of HLA-B7 supermotif bearing epitopes

The same target antigen protein sequences were also analyzed to identify HLA-B7-supermotif-bearing sequences. The corresponding peptides are then synthesized and tested for binding to HLA-B*0702, the most common B7-supertype allele (*i.e.*, the prototype B7 supertype allele). Those peptides that bind B*0702 with IC_{50} of ≤500 nM, preferably ≤ 200 nM, are then tested for binding to other common B7-supertype molecules (B*3501, B*5101, B*5301, and B*5401) to identify those peptides that are capable of binding to three or more of the five B7-supertype alleles tested.

Selection of A1 and A24 motif-bearing epitopes

To further increase population coverage, HLA-A1 and -A24 epitopes can also be incorporated into vaccine constructs. An analysis of the protein sequence data from the target antigens utilized above was performed to identify HLA-A1- and A24-motif-containing sequences. Peptides are then synthesized and tested for binding.

Peptides that bear other supermotifs and/or motifs can be assessed for binding or cross-reactive binding in an analogous manner.

Example 3. Confirmation of Immunogenicity

Cross-reactive candidate CTL A2-supermotif-bearing peptides that are identified as described in Example 2 were selected for *in vitro* immunogenicity testing. Examples of immunogenic HLA-A2 cross-reactive binding peptides that bind to at least 3/5 HLA-A2 supertype family members at an IC_{50} of 200 nM or less are shown in Table XXIV. Testing was performed using the following methodology:

Target Cell Lines for Cellular Screening:

The .221A2.1 cell line, produced by transferring the HLA-A2.1 gene into the HLA-A, -B, -C null mutant human B-lymphoblastoid cell line 721.221, is used as the peptide-loaded target to measure activity of HLA-A2.1-restricted CTL. This cell line is grown in RPMI-1640 medium supplemented with antibiotics, sodium pyruvate, nonessential amino acids and 10% (v/v) heat inactivated FCS. Cells that express an antigen of interest, or transfectants comprising the gene encoding the antigen of interest, can be used as target cells to test the ability of peptide-specific CTLs to recognize endogenous antigen.

Primary CTL Induction Cultures:

Generation of Dendritic Cells (DC): PBMCs are thawed in RPMI with 30 µg/ml DNAse, washed twice and resuspended in complete medium (RPMI-1640 plus 5% AB human serum, non-essential amino acids, sodium pyruvate, L-glutamine and penicillin/strpetomycin). The monocytes are purified by plating 10 x 10^6 PBMC/well in a 6-well plate. After 2 hours at 37°C, the non-adherent cells are removed by gently shaking the plates and aspirating the supernatants. The wells are washed a total of three times with 3 ml RPMI to remove most of the non-adherent and loosely adherent cells. Three ml of complete medium containing 50 ng/ml of GM-CSF and 1,000 U/ml of IL-4 are then added to each well. TNFα is added to the DCs on day 6 at 75 ng/ml and the cells are used for CTL induction cultures on day 7.

Induction of CTL with DC and Peptide: CD8+ T-cells are isolated by positive selection with Dynal immunomagnetic beads (Dynabeads® M-450) and the detacha-bead® reagent. Typically about 200-250x10^6 PBMC are processed to obtain 24x10^6 $CD8^+$ T-cells (enough for a 48-well plate culture). Briefly, the PBMCs are thawed in RPMI with 30µg/ml DNAse, washed once with PBS containing 1% human AB serum and resuspended in PBS/1% AB serum at a concentration of 20x10^6cells/ml. The magnetic beads are washed 3 times with PBS/AB serum, added to the cells (140µl beads/20x10^6 cells) and incubated for 1 hour at 4°C with continuous mixing. The beads and cells are washed 4x with PBS/AB serum to remove the nonadherent cells and resuspended at 100x10^6 cells/ml (based on the original cell number) in PBS/AB serum containing 100µl/ml detacha-bead® reagent and 30µg/ml DNAse. The mixture is incubated for 1 hour at room temperature with continuous mixing. The beads are washed again with PBS/AB/DNAse to collect the CD8+ T-cells. The DC are collected and centrifuged at 1300 rpm for 5-7 minutes, washed once with PBS with 1% BSA, counted and pulsed with 40µg/ml of peptide at a cell concentration of 1-2x10^6/ml in the presence of 3µg/ml $ß_2$- microglobulin for 4 hours at 20°C. The DC are then irradiated (4,200 rads), washed 1 time with medium and counted again.

Setting up induction cultures: 0.25 ml cytokine-generated DC (@1x10^5 cells/ml) are co-cultured with 0.25ml of CD8+ T-cells (@2x10^6 cell/ml) in each well of a 48-well plate in the presence of 10 ng/ml of IL-7. Recombinant human IL10 is added the

next day at a final concentration of 10 ng/ml and rhuman IL2 is added 48 hours later at 10IU/ml.

Restimulation of the induction cultures with peptide-pulsed adherent cells: Seven and fourteen days after the primary induction the cells are restimulated with peptide-pulsed adherent cells. The PBMCS are thawed and washed twice with RPMI and DNAse. The cells are resuspended at $5x10^6$ cells/ml and irradiated at ~4200 rads. The PBMCs are plated at $2x10^6$ in 0.5ml complete medium per well and incubated for 2 hours at 37°C. The plates are washed twice with RPMI by tapping the plate gently to remove the nonadherent cells and the adherent cells pulsed with 10μg/ml of peptide in the presence of 3 μg/ml $ß_2$ microglobulin in 0.25ml RPMI/5%AB per well for 2 hours at 37°C. Peptide solution from each well is aspirated and the wells are washed once with RPMI. Most of the media is aspirated from the induction cultures (CD8+ cells) and brought to 0.5 ml with fresh media. The cells are then transferred to the wells containing the peptide-pulsed adherent cells. Twenty four hours later rhuman IL10 is added at a final concentration of 10ng/ml and rhuman IL2 is added the next day and again 2-3 days later at 50IU/ml (Tsai *et al.*, *Critical Reviews in Immunology* 18(1-2):65-75, 1998). Seven days later the cultures are assayed for CTL activity in a ^{51}Cr release assay. In some experiments the cultures are assayed for peptide-specific recognition in the *in situ* IFNγ ELISA at the time of the second restimulation followed by assay of endogenous recognition 7 days later. After expansion, activity is measured in both assays for a side by side comparison.

Measurement of CTL lytic activity by ^{51}Cr release.

Seven days after the second restimulation, cytotoxicity is determined in a standard (5hr) ^{51}Cr release assay by assaying individual wells at a single E:T. Peptide-pulsed targets are prepared by incubating the cells with 10μg/ml peptide overnight at 37°C.

Adherent target cells are removed from culture flasks with trypsin-EDTA. Target cells are labelled with 200μCi of ^{51}Cr sodium chromate (Dupont, Wilmington, DE) for 1 hour at 37°C. Labelled target cells are resuspended at 10^6 per ml and diluted 1:10 with K562 cells at a concentration of $3.3x10^6$/ml (an NK-sensitive erythroblastoma cell line used to reduce non-specific lysis). Target cells (100 μl) and 100μl of effectors are plated in 96 well round-bottom plates and incubated for 5 hours at 37°C. At that time, 100 μl of supernatant are collected from each well and percent lysis is determined

according to the formula: [(cpm of the test sample- cpm of the spontaneous ^{51}Cr release sample)/(cpm of the maximal ^{51}Cr release sample- cpm of the spontaneous ^{51}Cr release sample)] x 100. Maximum and spontaneous release are determined by incubating the labelled targets with 1% Trition X-100 and media alone, respectively. A positive culture is defined as one in which the specific lysis (sample- background) is 10% or higher in the case of individual wells and is 15% or more at the 2 highest E:T ratios when expanded cultures are assayed.

***In situ* Measurement of Human γIFN Production as an Indicator of Peptide-specific and Endogenous Recognition**

Immulon 2 plates are coated with mouse anti-human IFNγ monoclonal antibody (4 μg/ml 0.1M $NaHCO_3$, pH8.2) overnight at 4°C. The plates are washed with Ca^{2+}, Mg^{2+}-free PBS/0.05% Tween 20 and blocked with PBS/10% FCS for 2 hours, after which the CTLs (100 μl/well) and targets (100 μl/well) are added to each well, leaving empty wells for the standards and blanks (which received media only). The target cells, either peptide-pulsed or endogenous targets, are used at a concentration of $1x10^6$ cells/ml. The plates are incubated for 48 hours at 37°C with 5% CO_2.

Recombinant human IFNγ is added to the standard wells starting at 400 pg or 1200pg/100μl/well and the plate incubated for 2 hours at 37°C. The plates are washed and 100 μl of biotinylated mouse anti-human IFNγ monoclonal antibody (2μg/ml in PBS/3%FCS/0.05% Tween 20) are added and incubated for 2 hours at room temperature. After washing again, 100 μl HRP-streptavidin (1:4000) are added and the plates incubated for 1 hour at room temperature. The plates are then washed 6x with wash buffer, 100μl/well developing solution (TMB 1:1) are added, and the plates allowed to develop for 5-15 minutes. The reaction is stopped with 50 μl/well 1M H_3PO_4 and read at OD450. A culture is considered positive if it measured at least 50 pg of IFNγ/well above background and is twice the background level of expression.

CTL Expansion. Those cultures that demonstrate specific lytic activity against peptide-pulsed targets and/or tumor targets are expanded over a two week period with anti-CD3. Briefly, $5x10^4$ CD8+ cells are added to a T25 flask containing the following: $1x10^6$ irradiated (4,200 rad) PBMC (autologous or allogeneic) per ml, $2x10^5$ irradiated (8,000 rad) EBV- transformed cells per ml, and OKT3 (anti-CD3) at 30ng per ml in RPMI-1640 containing 10% (v/v) human AB serum, non-essential amino acids,

sodium pyruvate, 25μM 2-mercaptoethanol, L-glutamine and penicillin/streptomycin. Rhuman IL2 is added 24 hours later at a final concentration of 200IU/ml and every 3 days thereafter with fresh media at 50IU/ml. The cells are split if the cell concentration exceeded $1x10^6$/ml and the cultures are assayed between days 13 and 15 at E:T ratios of 30, 10, 3 and 1:1 in the ^{51}Cr release assay or at $1x10^6$/ml in the *in situ* IFNγ assay using the same targets as before the expansion.

Cultures are expanded in the absence of anti-$CD3^+$ as follows. Those cultures that demonstrate specific lytic activity against peptide and endogenous targets are selected and $5x10^4$ $CD8^+$ cells are added to a T25 flask containing the following: $1x10^6$ autologous PBMC per ml which have been peptide-pulsed with 10μg/ml peptide for 2 hours at 37°C and irradiated (4,200 rad); $2x10^5$ irradiated (8,000 rad) EBV-transformed cells per ml RPMI-1640 containing 10%(v/v) human AB serum, non-essential AA, sodium pyruvate, 25mM 2-ME, L-glutamine and gentamicin.

Immunogenicity of A2 supermotif-bearing peptides

A2-supermotif cross-reactive binding peptides were tested in the cellular assay for the ability to induce peptide-specific CTL in normal individuals. In this analysis, a peptide is considered to be an epitope if it induces peptide-specific CTLs in at least 2 donors (unless otherwise noted) and preferably, also recognizes the endogenously expressed peptide. Examples of immunogenic peptides are shown in Table XXIV.

Immunogenicity is additionally confirmed using PBMCs isolated from cancer patients. Briefly, PBMCs are isolated from patients with prostate cancer, re-stimulated with peptide-pulsed monocytes and assayed for the ability to recognize peptide-pulsed target cells as well as transfected cells endogenously expressing the antigen.

*Evaluation of A*03/A11 immunogenicity*

HLA-A3 supermotif-bearing cross-reactive binding peptides are also evaluated for immunogenicity using methodology analogous for that used to evaluate the immunogenicity of the HLA-A2 supermotif peptides.

Evaluation of B7 immunogenicity

Immunogenicity screening of the B7-supertype cross-reactive binding peptides identified in Example 2 are evaluated in a manner analogous to the evaluation of A2-and A3-supermotif-bearing peptides.

Peptides bearing other supermotifs and/or motifs, *e.g.*, HLA-A1, HLA-a24 *etc.* are also evaluated using similar methodology

Example 4. Implementation of the Extended Supermotif to Improve the Binding Capacity of Native Epitopes by Creating Analogs

HLA motifs and supermotifs (comprising primary and/or secondary residues) are useful in the identification and preparation of highly cross-reactive native peptides, as demonstrated herein. Moreover, the definition of HLA motifs and supermotifs also allows one to engineer highly cross-reactive epitopes by identifying residues within a native peptide sequence which can be analoged, or "fixed" to confer upon the peptide certain characteristics, *e.g.* greater cross-reactivity within the group of HLA molecules that comprise a supertype, and/or greater binding affinity for some or all of those HLA molecules. Examples of analog peptides that exhibit modulated binding affinity are set forth in this example.

Analoging at Primary Anchor Residues

Peptide engineering strategies were implemented to further increase the cross-reactivity of the epitopes identified above (*see, e.g.*, Table XXIII). On the basis of the data disclosed, *e.g.*, in related and co-pending U.S.S.N 09/226,775, the main anchors of A2-supermotif-bearing peptides are altered, for example, to introduce a preferred L, I, V, or M at position 2, and I or V at the C-terminus.

Peptides that exhibit at least weak A*0201 binding (IC_{50} of 5000 nM or less), and carrying suboptimal anchor residues at either position 2, the C-terminal position, or both, can be fixed by introducing canonical substitutions (typically L at position 2 and V at the C-terminus). Those analoged peptides that show at least a three-fold increase in A*0201 binding and bind with an IC_{50} of 500 nM, or preferably 200 nM, or less are then tested for A2 cross-reactive binding along with their wild-type (WT) counterparts. Analoged peptides that bind at least three of the five A2 supertype alleles are then selected for cellular screening analysis.

Additionally, the selection of analogs for cellular screening analysis is further restricted by the capacity of the WT parent peptide to bind at least weakly, *i.e.*, bind at an IC_{50} of 5000nM or less, to three of more A2 supertype alleles. The rationale for this requirement is that the WT peptides must be present endogenously in sufficient quantity to be biologically relevant. Analoged peptides have been shown to have increased immunogenicity and cross-reactivity by T cells specific for the WT epitope (*see, e.g.*, Parkhurst *et al.*, *J. Immunol.* 157:2539, 1996; and Pogue *et al.*, *Proc. Natl. Acad. Sci. USA* 92:8166, 1995).

In the cellular screening of these peptide analogs, it is important to demonstrate that analog-specific CTLs are also able to recognize the wild-type peptide and, when possible, tumor targets that endogenously express the epitope.

Peptides that were analoged at primary anchor residues, generally by adding a preferred resiude at a primary anchor position, were synthesized and assessed for enhanced binding to A*0201 and/or enhanced cross-reactive binding. Examples of analoged peptides that exhibit increased binding and/or cross-reactivity are shown in Table XXIII.

Analogs exhibiting altered binding characteristics are then selected for cellular screening studies. Examples are shown in Table XXIV.

Using methodology similar to that used to develop HLA-A2 analogs, analogs of HLA-A3 and HLA-B7 supermotif-bearing epitopes are also generated. Analogous strategies can be used for peptides bearing other supermotifs/motifs as well. For example, peptides binding at least weakly to 3/5 of the A3-supertype molecules may be engineered at primary anchor residues to possess a preferred residue (V, S, M, or A) at position 2. The analog peptides are then tested for the ability to bind A*03 and A*11 (prototype A3 supertype alleles). Those peptides that demonstrate ≤ 500 nM binding capacity, often ≤ 200 nM binding values, are then tested for A3-supertype cross-reactivity. B7 supermotif-bearing peptides may, for example, be engineered to possess a preferred residue (V, I, L, or F) at the C-terminal primary anchor position, as demonstrated by Sidney *et al.* (*J. Immunol.* 157:3480-3490, 1996) and tested for binding to B7 supertype alleles.

Analoging at Secondary Anchor Residues

Moreover, HLA supermotifs are of value in engineering highly cross-reactive peptides and/or peptides that bind HLA molecules with increased affinity by

identifying particular residues at secondary anchor positions that are associated with such properties. For example, the binding capacity of a B7 supermotif-bearing peptide representing a discreet single amino acid substitution at position 1 can be analyzed. A peptide can, for example, be analoged to substitute L with F at position 1 and subsequently be evaluated for increased binding affinity/ and or increased cross-reactivity. This procedure will identify analoged peptides with modulated binding affinity.

Engineered analogs with sufficiently improved binding capacity or cross-reactivity are tested for immunogenicity as above.

Other analoging strategies

Another form of peptide analoging, unrelated to the anchor positions, involves the substitution of a cysteine with α-amino butyric acid. Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Subtitution of α-amino butyric acid for cysteine not only alleviates this problem, but has been shown to improve binding and crossbinding capabilities in some instances (*see, e.g.*, the review by Sette *et al.*, In: Persistent Viral Infections, Eds. R. Ahmed and I. Chen, John Wiley & Sons, England, 1999).

In conclusion, these data demonstrate that by the use of even single amino acid substitutions, it is possible to increase the binding affinity and/or cross-reactivity of peptide ligands for HLA supertype molecules.

Example 5. Identification of peptide epitope sequences with HLA-DR binding motifs

Peptide epitopes bearing an HLA class II supermotif or motif may also be identified as outlined below using methodology similar to that described in Examples 1-3.

Selection of HLA-DR-supermotif-bearing epitopes

To identify HLA class II HTL epitopes, the prostate cancer-associate antigen protein sequences were analyzed for the presence of sequences bearing an HLA-DR-motif or supermotif. Specifically, 15-mer sequences are selected comprising a DR-supermotif, further comprising a 9-mer core, and three-residue N- and C-terminal flanking regions (15 amino acids total).

Protocols for predicting peptide binding to DR molecules have been developed (Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). These protocols, specific for individual DR molecules, allow the scoring, and ranking, of 9-mer core regions. Each protocol not only scores peptide sequences for the presence of DR-supermotif primary anchors (i.e., at position 1 and position 6) within a 9-mer core, but additionally evaluates sequences for the presence of secondary anchors. Using allele specific selection tables (*see, e.g.*, Southwood *et al.*, *ibid.*), it has been found that these protocols efficiently select peptide sequences with a high probability of binding a particular DR molecule. Additionally, it has been found that performing these protocols in tandem, specifically those for DR1, DR4w4, and DR7, can efficiently select DR cross-reactive peptides.

The prostate antigen-derived peptides identified above are tested for their binding capacity to various common HLA-DR molecules. All peptides are initially tested for binding to the DR molecules in the primary panel: DR1, DR4w4, and DR7. Peptides binding at least 2 of these 3 DR molecules with an IC_{50} value of 1000 nM or less, were then tested for binding to DR5*0101, DRB1*1501, DRB1*1101, DRB1*0802, and DRB1*1302. Peptides were considered to be cross-reactive DR supertype binders if they bound at an IC_{50} value of 1000 nM or less to at least 5 of the 8 alleles tested.

Following the strategy outlined above DR supermotif-bearing sequences were identified within the prostate antigen protein sequence. Generally, these sequences are then scored for the combined DR 1-4-7 algorithms. The postive-scoring peptides are synthesized and tested for binding to HLA-DRB1*0101, DRB1*0401, DRB1*0701. Those that bind at least 2 of the 3 alleles are then tested for binding to secondary DR supertype alleles: DRB5*0101, DRB1*1501, DRB1*1101, DRB1*0802, and DRB1*1302.

Selection of DR3 motif peptides

Because HLA-DR3 is an allele that is prevalent in Caucasian, Black, and Hispanic populations, DR3 binding capacity is an important criterion in the selection of HTL epitopes. However, data generated previously indicated that DR3 only rarely cross-reacts with other DR alleles (Sidney *et al., J. Immunol.* 149:2634-2640, 1992; Geluk *et al.*, *J. Immunol.* 152:5742-5748, 1994; Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). This is not entirely surprising in that the DR3 peptide-binding motif appears to be distinct from the specificity of most other DR alleles. For maximum efficiency in

developing vaccine candidates it would be desirable for DR3 motifs to be clustered in proximity with DR supermotif regions. Thus, peptides shown to be candidates may also be assayed for their DR3 binding capacity. However, in view of the distinct binding specificity of the DR3 motif, peptides binding only to DR3 can also be considered as candidates for inclusion in a vaccine formulation.

To efficiently identify peptides that bind DR3, the PSA, PSM, PAP, and hK2 protein sequences were analyzed for sequences carrying one of the two DR3 specific binding motifs (Table III) reported by Geluk *et al.* (*J. Immunol.* 152:5742-5748, 1994). The corresponding peptides are then synthesized and tested for the ability to bind DR3 with an affinity of 1000 nM or better, *i.e.*, less than 1000 nM.

Additionally, the DR3 binders are also tested for binding to the DR supertype alleles. Conversely, the DR supertype cross-reactive binding peptides are also tested for DR3 binding capacity.

DR3 binding epitopes identified in this manner are then included in vaccine compositions with DR supermotif-bearing peptide epitopes.

Similarly to the case of HLA class I motif-bearing peptides, the class II motif-bearing peptides are analoged to improve affinity or cross-reactivity. For example, aspartic acid at position 4 of the 9-mer core sequence is an optimal residue for DR3 binding, and substitution for that residue often improves DR 3 binding.

For example, a number of HLA-DR supermotif and DR-3 motif-bearing prostate antigen-associated sequences have been identified. The number in each category is summarized in Table XXV.

Example 6. Immunogenicity of HTL epitopes

This example determines immunogenic DR supermotif- and DR3 motif-bearing epitopes among those identified using the methodology in Example 5.

Immunogenicity of HTL epitopes are evaluated in a manner analogous to the determination of immunogenicity of CTL epitopes by assessing the ability to stimulate HTL responses and/or by using appropriate transgenic mouse models. Immunogenicity is determined by screening for: 1.) *in vitro* primary induction using normal PBMC or 2.) recall responses from cancer patient PBMCs.

Example 7. Calculation of phenotypic frequencies of HLA-supertypes in various ethnic backgrounds to determine breadth of population coverage

This example illustrates the assessment of the breadth of population coverage of a vaccine composition comprised of multiple epitopes comprising multiple supermotifs and/or motifs.

In order to analyze population coverage, gene frequencies of HLA alleles were determined. Gene frequencies for each HLA allele were calculated from antigen or allele frequencies utilizing the binomial distribution formulae gf=1-(SQRT(1-af)) (see, *e.g.*, Sidney *et al.*, *Human Immunol.* 45:79-93, 1996). To obtain overall phenotypic frequencies, cumulative gene frequencies were calculated, and the cumulative antigen frequencies derived by the use of the inverse formula [af=1-(1-Cgf)^2].

Where frequency data was not available at the level of DNA typing, correspondence to the serologically defined antigen frequencies was assumed. To obtain total potential supertype population coverage no linkage disequilibrium was assumed, and only alleles confirmed to belong to each of the supertypes were included (minimal estimates). Estimates of total potential coverage achieved by inter-loci combinations were made by adding to the A coverage the proportion of the non-A covered population that could be expected to be covered by the B alleles considered (*e.g.*, total=A+B*(1-A)). Confirmed members of the A3-like supertype are A3, A11, A31, A*3301, and A*6801. Although the A3-like supertype may also include A34, A66, and A*7401, these alleles were not included in overall frequency calculations. Likewise, confirmed members of the A2-like supertype family are A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*6802, and A*6901. Finally, the B7-like supertype-confirmed alleles are: B7, B*3501-03, B51, B*5301, B*5401, B*5501-2, B*5601, B*6701, and B*7801 (potentially also B*1401, B*3504-06, B*4201, and B*5602).

Population coverage achieved by combining the A2-, A3- and B7-supertypes is approximately 86% in five major ethnic groups (see Table XXI). Coverage may be extended by including peptides bearing the A1 and A24 motifs. On average, A1 is present in 12% and A24 in 29% of the population across five different major ethnic groups (Caucasian, North American Black, Chinese, Japanese, and Hispanic). Together, these alleles are represented with an average frequency of 39% in these same ethnic populations. The total coverage across the major ethnicities when A1 and A24 are combined with the coverage of the A2-, A3- and B7-supertype alleles is >95%. An

analogous approach can be used to estimate population coverage achieved with combinations of class II motif-bearing epitopes.

Example 8. Recognition Of Generation Of Endogenous Processed Antigens After Priming

This example determines that CTL induced by native or analogued peptide epitopes identified and selected as described in Examples 1-6 recognize endogenously synthesized, *i.e.*, native antigens, using a transgenic mouse model.

Effector cells isolated from transgenic mice that are immunized with peptide epitopes (as described, *e.g.*, in Wentworth et al., *Mol. Immunol.* 32:603, 1995), for example HLA-A2 supermotif-bearing epitopes, are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on ^{51}Cr labeled Jurkat-A2.1/K^b target cells in the absence or presence of peptide, and also tested on ^{51}Cr labeled target cells bearing the endogenously synthesized antigen, *i.e.* prostate tumor cells or cells that are stably transfected with TAA expression vectors.

The result will demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that is being evaluated. In addition to HLA-A*0201/K^b transgenic mice, several other transgenic mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

Example 9. Activity Of CTL-HTL Conjugated Epitopes In Transgenic Mice

This example illustrates the induction of CTLs and HTLs in transgenic mice by use of a tumor associated antigen CTL/HTL peptide conjugate whereby the vaccine composition comprises peptides to be administered to a cancer patient. The peptide composition can comprise multiple CTL and/or HTL epitopes and further, can comprise epitopes selected from multiple-tumor associated antigens. The epitopes are identified using methodology as described in Examples 1-6 This analysis demonstrates the enhanced immunogenicity that can be achieved by inclusion of one or more HTL

epitopes in a vaccine composition. Such a peptide composition can comprise an HTL epitope conjugated to a preferred CTL epitope containing, for example, at least one CTL epitope selected from Table XXIII, or other analogs of that epitope. The peptides may be lipidated, if desired.

Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K^b mice, which are transgenic for the human HLA A2.1 allele and are useful for the assessment of the immunogenicity of HLA-A*0201 motif- or HLA-A2 supermotif-bearing epitopes, are primed subcutaneously (base of the tail) with a 0.1 ml of peptide in Incomplete Freund's Adjuvant, or if the peptide composition is a lipidated CTL/HTL conjugate, in DMSO/saline or if the peptide composition is a polypeptide, in PBS or Incomplete Freund's Adjuvant. Seven days after priming, splenocytes obtained from these animals are restimulated with syngenic irradiated LPS-activated lymphoblasts coated with peptide.

The target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (*e.g.*, Vitiello *et al., J. Exp. Med.* 173:1007, 1991).

In vitro CTL activation: One week after priming, spleen cells ($30x10^6$ cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated lymphoblasts ($10x10^6$ cells/flask) in 10 ml of culture medium/T25 flask. After six days, effector cells are harvested and assayed for cytotoxic activity.

Assay for cytotoxic activity: Target cells (1.0 to $1.5x10^6$) are incubated at 37°C in the presence of 200 µl of ^{51}Cr. After 60 minutes, cells are washed three times and resuspended in medium. Peptide is added where required at a concentration of 1 µg/ml. For the assay, 10^4 ^{51}Cr-labeled target cells are added to different concentrations of effector cells (final volume of 200 µl) in U-bottom 96-well plates. After a 6 hour incubation period at 37°C, a 0.1 ml aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release = 100 x (experimental release - spontaneous release)/(maximum release - spontaneous release). To facilitate comparison between separate CTL assays run under the same conditions, % ^{51}Cr release data is expressed as lytic units/10^6 cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a 6 hour ^{51}Cr release assay. To obtain specific lytic units/10^6, the lytic units/10^6 obtained in

the absence of peptide is subtracted from the lytic units/10^6 obtained in the presence of peptide. For example, if 30% ^{51}Cr release is obtained at the effector (E): target (T) ratio of 50:1 (i.e., $5x10^5$ effector cells for 10,000 targets) in the absence of peptide and 5:1 (i.e., $5x10^4$ effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be: $[(1/50,000)-(1/500,000)] \times 10^6 = 18$ LU.

The results are analyzed to assess the magnitude of the CTL responses of animals injected with the immunogenic CTL/HTL conjugate vaccine preparation. The magnitude and frequency of the response can also be compared to the the CTL response achieved using the CTL epitopes by themselves. Analyses similar to this may be performed to evaluate the immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures it is found that a CTL response is induced, and concomitantly that an HTL response is induced upon administration of such compositions.

Example 10. Selection of CTL and HTL epitopes for inclusion in a cancer vaccine.

This example illustrates the procedure for the selection of peptide epitopes for vaccine compositions of the invention. The peptides in the composition can be in the form of a nucleic acid sequence, either single or one or more sequences (*i.e.*, minigene) that encodes peptide(s), or may be single and/or polyepitopic peptides.

The following principles are utilized when selecting an array of epitopes for inclusion in a vaccine composition. Each of the following principles is balanced in order to make the selection.

Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with tumor clearance. For example, a vaccine can include 3-4 epitopes that come from at least one prostate cancer-associated antigen. Epitopes from one prostate cancer-associated antigen can be used in combination with epitopes from one or more additional TAAs to produce a vaccine that targets tumors with varying expression patterns of frequently-expressed TAAs as described, *e.g.*, in Example 15.

Epitopes are preferably selected that have a binding affinity (IC_{50}) of 500 nM or less, often 200 nM or less, for an HLA class I molecule, or for a class II molecule, 1000 nM or less.

Sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. For example, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess breadth, or redundancy, of population coverage.

When selecting epitopes from cancer-related antigens it is often preferred to select analogs because the patient may have developed tolerance to the native epitope.

When creating a polyepitopic composition, *e.g.* a minigene, it is typically desirable to generate the smallest peptide possible that encompasses the epitopes of interest, although spacers or other flanking sequences can also be incorporated. The principles employed are often similar as those employed when selecting a peptide comprising nested epitopes. Additionally, however, upon determination of the nucleic acid sequence to be provided as a minigene, the peptide sequence encoded thereby is analyzed to determine whether any "junctional epitopes" have been created. A junctional epitope is a potential HLA binding epitope, as predicted, *e.g.*, by motif analysis. Junctional epitopes are generally to be avoided because the recipient may bind to an HLA molecule and generate an immune response to that epitope, which is not present in a native protein sequence.

A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response that results in tumor cell killing and reduction of tumor size or mass.

Example 11. Construction of Minigene Multi-Epitope DNA Plasmids

This example provides general guidance for the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of CTL and/or HTL epitopes or epitope analogs as described herein. Examples of the construction and evaluation of expression plasmids are described, for example, in co-pending U.S.S.N. 09/311,784 filed 5/13/99.

A minigene expression plasmid may include multiple CTL and HTL peptide epitopes. In this example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes. HLA class I supermotif or motif-bearing peptide epitopes derived from multiple prostate cancer-associated antigens are selected such that multiple supermotifs/motifs are represented to ensure broad

population coverage. Similarly, HLA class II epitopes are selected from multiple prostate cancer-associated antigens to provide broad population coverage, *i.e.* both HLA DR-1-4-7 supermotif-bearing epitopes and HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct. The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

This example illustrates the methods to be used for construction of such a minigene-bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

The minigene DNA plasmid contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance with principles disclosed herein. The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

Overlapping oligonucleotides that can, for example, average about 70 nucleotides in length with 15 nucleotide overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multiepitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing temperature (5° below the lowest calculated Tm of each primer pair) for 30 sec, and 72°C for 1 min.

For example, a minigene can be prepared as follows. For a first PCR reaction, 5 μg of each of two oligonucleotides are annealed and extended: In an example using eight oligonucleotides, *i.e.*, four pairs of primers, oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 μl reactions containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM $(NH_4)_2SO_4$, 20 mM Tris-chloride, pH 8.75, 2 mM $MgSO_4$, 0.1% Triton X-100, 100 μg/ml BSA), 0.25 mM each dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to amplify the full length product. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

Example 12. The plasmid construct and the degree to which it induces immunogenicity.

The degree to which a plasmid construct, for example a plasmid constructed in accordance with Example 11, is able to induce immunogenicity can be evaluated *in vitro* by testing for epitope presentation by APC following transduction or transfection of the APC with an epitope-expressing nucleic acid construct. Such a study determines "antigenicity" and allows the use of human APC. The assay determines the ability of the epitope to be presented by the APC in a context that is recognized by a T cell by quantifying the density of epitope-HLA class I complexes on the cell surface. Quantitation can be performed by directly measuring the amount of peptide eluted from the APC (*see, e.g.*, Sijts *et al.*, *J. Immunol.* 156:683-692, 1996; Demotz *et al.*, *Nature* 342:682-684, 1989); or the number of peptide-HLA class I complexes can be estimated by measuring the amount of lysis or lymphokine release induced by infected or transfected target cells, and then determining the concentration of peptide necessary to obtained equivalent levels of lysis or lymphokine release (*see, e.g.*, Kageyama *et al.*, *J. Immunol.* 154:567-576, 1995).

Atlernatively, immunogenicity can be evaluated through *in vivo* injections into mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analysed using cytotoxicity and proliferation assays, respectively, as detailed *e.g.*, in co-pending U.S.S.N. 09/311,784 filed 5/13/99 and Alexander *et al.*, *Immunity* 1:751-761, 1994.

For example, to assess the capacity of a DNA minigene construct (*e.g.*, a pMin minigene construct generated as decribed in U.S.S.N. 09/311,784) containing at least one HLA-A2 supermotif peptide to induce CTLs *in vivo*, HLA-A2.1/K^b transgenic mice, for example, are immunized intramuscularly with 100 µg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA immunization, a control group of animals is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.

Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polyepitopic peptide), then assayed for peptide-specific cytotoxic activity in a ^{51}Cr release assay. The results indicate the magnitude of the CTL response directed against the A2-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polyepitopic vaccine. It is, therefore, found that the minigene elicits immune responses directed toward the HLA-A2 supermotif peptide epitopes as does the polyepitopic peptide

vaccine. A similar analysis is also performed using other HLA-A3 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes.

To assess the capacity of a class II epitope encoding minigene to induce HTLs *in vivo*, DR transgenic mice, or for those epitope that cross react with the appropriate mouse MHC molecule, I-A^b-restricted mice, for example, are immunized intramuscularly with 100 µg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant. CD4+ T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene). The HTL response is measured using a ^{3}H-thymidine incorporation proliferation assay, (*see, e.g.*, Alexander et al. Immunity 1:751-761, 1994). The results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

DNA minigenes, constructed as described in Example 11, may also be evaluated as a vaccine in combination with a boosting agent using a prime boost protocol. The boosting agent can consist of recombinant protein (*e.g.*, Barnett *et al.*, *Aids Res. and Human Retroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (*see, e.g.*, Hanke *et al.*, *Vaccine* 16:439-445, 1998; Sedegah *et al.*, *Proc. Natl. Acad. Sci USA* 95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson *et al.*, *Nature Med.* 5:526-34, 1999).

For example, the efficacy of the DNA minigene used in a prime boost protocol is initially evaluated in transgenic mice. In this example, A2.1/K^b transgenic mice are immunized IM with 100 µg of a DNA minigene encoding the immunogenic peptides including at least one HLA-A2 supermotif-bearing peptide. After an incubation period (ranging from 3-9 weeks), the mice are boosted IP with 10^7 pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 µg of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the

minigene and recombinant vaccinia, then assayed for peptide-specific activity in an IFN-γ ELISA.

It is found that the minigene utilized in a prime-boost protocol elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis can also be performed using HLA-A11 or HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 or HLA-B7 motif or supermotif epitopes.

The use of prime boost protocols in humans is described in Example 20.

Example 13. Peptide Composition for Prophylactic Uses

Vaccine compositions of the present invention are used to prevent cancer in persons who are at high risk for developing a tumor. For example, a polyepitopic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes such as those selected in Examples 9 and/or 10, which are also selected to target greater than 80% of the population, is administered to an individual at high risk for prostate cancer. The composition is provided as a single polypeptide that encompasses multiple epitopes. The vaccine is administered in an aqueous carrier comprised of Freunds Incomplete Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 μg, generally 100-5,000 μg, for a 70 kg patient. The initial administration of vaccine is followed by booster dosages at 4 weeks followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against cancer.

Alternatively, the polyepitopic peptide composition can be administered as a nucleic acid in accordance with methodologies known in the art and disclosed herein.

Example 14. Polyepitopic Vaccine Compositions Derived from Native TAA Sequences

A native TAA polyprotein sequence is screened, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify "relatively short" regions of the polyprotein that comprise multiple epitopes and is preferably less in length than an entire native antigen. This relatively short sequence that contains multiple distinct, even overlapping, epitopes is selected and used to generate a minigene construct. The construct is engineered to express the peptide, which

corresponds to the native protein sequence. The "relatively short" peptide is generally less than 1000, 500, or 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping (*i.e.*, frame shifted relative to one another). For example, with frame shifted overlapping epitopes, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes.

The vaccine composition will preferably include, for example, three CTL epitopes and at least one HTL epitope from multiple prostate cancer-associated antigens. This polyepitopic native sequence is administered either as a peptide or as a nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide.

The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent analogs) directs the immune response to multiple peptide sequences that are actually present in native TAAs thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions.

Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of epitopes per sequence length.

Example 15. Polyepitopic Vaccine Compositions Comprising Epitopes From Multiple Tumor-Associated Antigens

The prostate cancer-associated antigen peptide epitopes of the present invention are used in combination with each other, or with peptide epitopes from other target tumor-associated antigens to create a vaccine composition that is useful for the

treatment of prostate tumors from multiple patients. Furthermore, a vaccine composition comprising epitopes from multiple tumor antigens also reduces the potential for escape mutants due to loss of expression of an individual tumor antigen.

The composition can be provided as a single polypeptide that incorporates the multiple epitopes from the various TAAs, or can be administered as a composition comprising one or more discrete epitopes. Alternatively, the vaccine can be administered as a minigene construct or as dendritic cells which have been loaded with the peptide epitopes *in vitro*.

Example 16. Use of peptides to evaluate an immune response

Peptides of the invention may be used to analyze an immune response for the presence of specific CTL or HTL populations directed to a prostate cancer-associated antigen. Such an analysis may be performed using multimeric complexes as described, *e.g.*, by Ogg *et al., Science* 279:2103-2106, 1998 and Greten *et al., Proc. Natl. Acad. Sci. USA* 95:7568-7573, 1998. In the following example, peptides in accordance with the invention are used as a reagent for diagnostic or prognostic purposes, not as an immunogen.

In this example, highly sensitive human leukocyte antigen tetrameric complexes ("tetramers") are used for a cross-sectional analysis of, for example, tumor-associated antigen HLA-A*0201-specific CTL frequencies from HLA A*0201-positive individuals at different stages of disease or following immunization using a TAA peptide containing an A*0201 motif. Tetrameric complexes are synthesized as described (Musey *et al., N. Engl. J. Med.* 337:1267, 1997). Briefly, purified HLA heavy chain (A*0201 in this example) and β2-microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain, β2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5'triphosphate and magnesium. Streptavidin-phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300g for 5 minutes and resuspended in 50 µl of cold phosphate-buffered saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are applied to contain >99.98% of control samples. Controls for the tetramers include both A*0201-negative individuals and A*0201-positive uninfected donors. The percentage of cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby readily indicating the extent of immune response to the TAA epitope, and thus the stage of tumor progression or exposure to a vaccine that elicits a protective or therapeutic response.

Example 17. Use of Peptide Epitopes to Evaluate Recall Responses

The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who are in remission, have a tumor, or who have been vaccinated with a prostate cancer-associated antigen vaccine.

For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any TAA vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA supertype family members, are then used for analysis of samples derived from individuals who bear that HLA type.

PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 µg/ml), and Hepes (10mM) containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is added at 10 µg/ml to each well and HBV core 128-140 epitope is added at 1 µg/ml to each well as a source of T cell help during the first week of stimulation.

In the microculture format, 4 x 10^5 PBMC are stimulated with peptide in 8 replicate cultures in 96-well round bottom plate in 100 µl/well of complete RPMI. On

days 3 and 10, 100 µl of complete RPMI and 20 U/ml final concentration of rIL-2 are added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and 10^5 irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response requires two or more of the eight replicate cultures to display greater than 10% specific ^{51}Cr release, based on comparison with uninfected control subjects as previously described (Rehermann, *et al., Nature Med.* 2:1104,1108, 1996; Rehermann *et al., J. Clin. Invest.* 97:1655-1665, 1996; and Rehermann *et al. J. Clin. Invest.* 98:1432-1440, 1996).

Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics (ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al. J. Virol. 66*:2670-2678, 1992).

Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10 µM, and labeled with 100 µCi of ^{51}Cr (Amersham Corp., Arlington Heights, IL) for 1 hour after which they are washed four times with HBSS.

Cytolytic activity is determined in a standard 4 hour, split-well ^{51}Cr release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula: 100 x [(experimental release-spontaneous release)/maximum release-spontaneous release)]. Maximum release is determined by lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to the TAA or TAA vaccine.

The class II restricted HTL responses may also be analyzed. Purified PBMC are cultured in a 96-well flat bottom plate at a density of $1.5x10^5$ cells/well and are stimulated with 10 µg/ml synthetic peptide, whole antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1 µCi ^3H-thymidine is added to each well and incubation is continued for an additional 18 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for

^{3}H-thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of ^{3}H-thymidine incorporation in the presence of antigen divided by the ^{3}H-thymidine incorporation in the absence of antigen.

Example 18. Induction Of Specific CTL Response In Humans

A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study. Such a trial is designed, for example, as follows:

A total of about 27 male subjects are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 μg of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 μg peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 μg of peptide composition.

After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage. Additional booster inoculations can be administered on the same schedule.

The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the peptide composition are an index of the intrinsic activity of the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.

Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.

Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

The vaccine is found to be both safe and efficacious.

Example 19. Therapeutic Use in Cancer Patients

Evaluation of vaccine compositions are performed to validate the efficacy of the CTL-HTL peptide compositions in cancer patients. The main objectives of the trials are to determine an effective dose and regimen for inducing CTLs in prostate cancer patients, to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of cancer patients, as manifested by a reduction in tumor cell numbers. Such a study is designed, for example, as follows:

The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.

There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group are males, typically above the age of 50, and represent diverse ethnic backgrounds.

Example 20. Induction of CTL Responses Using a Prime Boost Protocol

A prime boost protocol similar in its underlying principle to that used to evaluate the efficacy of a DNA vaccine in transgenic mice, such as described in Example 12, can also be used for the administration of the vaccine to humans. Such a vaccine regimen can include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.

For example, the initial immunization can be performed using an expression vector, such as one constructed in accordance with Example 11, in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 μg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster can be recombinant fowlpox virus administered at a dose of $5\text{-}10^7$ to $5\text{x}10^9$ pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polyepitopic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood

samples will be obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

Analysis of the results will indicate that a magnitude of response sufficient to achieve protective immunity against prostate cancer is generated.

Example 21. Administration of Vaccine Compositions Using Antigen Presenting Cells

Vaccines comprising peptide epitopes of the invention may be administered using antigen-presenting cells (APCs), or "professional" APCs such as dendritic cells (DC). In this example, the peptide-pulsed DC are administered to a patient to stimulate a CTL response *in vivo*. In this method, dendritic cells are isolated, expanded, and pulsed with a vaccine comprising peptide CTL and HTL epitopes of the invention. The dendritic cells are infused back into the patient to elicit CTL and HTL responses *in vivo*. The induced CTL and HTL then destroy (CTL) or facilitate destruction (HTL) of the specific target tumor cells that bear the proteins from which the epitopes in the vaccine are derived.

For example, a cocktail of epitope-bearing peptides is administered *ex vivo* to PBMC, or isolated DC therefrom, from the patient's blood. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides.

As appreciated clinically, and readily determined by one of skill based on clinical outcomes, the number of dendritic cells reinfused into the patient can vary (*see, e.g.*, *Nature Med.* 4:328, 1998; *Nature Med.* 2:52, 1996 and *Prostate* 32:272, 1997). Although 2-50 x 10^6 dendritic cells per patient are typically administered, larger number of dendritic cells, such as 10^7 or 10^8 can also be provided. Such cell populations typically contain between 50-90% dendritic cells.

In some embodiments, peptide-loaded PBMC are injected into patients without purification of the DC. For example, PBMC containing DC generated after treatment with an agent such as Progenipoietin™ are injected into patients without purification of the DC. The total number of PBMC that are administered often ranges from 10^8 to 10^{10}. Generally, the cell doses injected into patients is based on the

percentage of DC in the blood of each patient, as determined, for example, by immunofluorescence analysis with specific anti-DC antibodies. Thus, for example, if Progenipoietin™ mobilizes 2% DC in the peripheral blood of a given patient, and that patient is to receive 5 x 10^6 DC, then the patient will be injected with a total of 2.5 x 10^8 peptide-loaded PBMC. The percent DC mobilized by an agent such as Progenipoietin™ is typically estimated to be between 2-10%, but can vary as appreciated by one of skill in the art.

The ability of DC to stimulate immune responses was evaluated in both *in vitro* and *in vivo* immune function assays. These assays include the stimulation of CTL hybridomas and CTL cell lines, and the *in vivo* activation of CTL.

DC Purification

Progenipoietin™-mobilized DC were purified from peripheral blood (PB) and spleens of Progenipoietin™-treated C57Bl/6 mice to evaluate their ability to present antigen and to elicit cellular immune responses. Briefly, DC were purified from total WBC and spleen using a positive selection strategy employing magnetic beads coated with a CD11c specific antibody (Miltenyi Biotec, Auburn CA). For comparison, *ex vivo* expanded DC were generated by culturing bone marrow cells from untreated C57Bl/6 mice with the standard cocktail of GM-CSF and IL-4 (R&D Systems, Minneapolis, MN) for a period of 7-8 days (Mayordomo *et al., Nature Med.* 1:1297-1302 (1995)). Recent studies have revealed that this *ex vivo* expanded DC population contains effective antigen presenting cells, with the capacity to stimulate anti-tumor immune responses (Celluzzi *et al., J. Exp. Med.* 83:283-287 (1996)).

The purities of Progenipoietin™-derived DC (100 μg/day, 10 days, SC) and GM-CSF/IL-4 *ex vivo* expanded DC were determined by flow cytometry. DC populations were defined as cells expressing both CD11c and MHC Class II molecules. Following purification of DC from magnetic CD11c microbeads, the percentage of double positive PB-derived DC, isolated from Progenipoietin™-treated mice, was enriched from approximately 4% to a range from 48-57% (average yield = 4.5 x 10^6 DC/animal). The percentage of purified splenic DC isolated from Progenipoietin™ treated mice was enriched from a range of 12-17% to a range of 67-77%. The purity of GM-CSF/IL-4 *ex vivo* expanded DC ranged from 31-41% (Wong *et al.*, *J. Immunother.*, 21:32040 (1998)).

In Vitro Stimulation of CTL Hybridomas and CTL Cell Lines: Presentation of Specific CTL Epitopes

The ability of Progenipoietin™ generated DC to stimulate a CTL cell line was demonstrated *in vitro* using a viral-derived epitope and a corresponding epitope responsive CTL cell line. Transgenic mice expressing human HLA-A2.1 were treated with Progenipoietin™. Splenic DC isolated from these mice were pulsed with a peptide epitope derived from hepatitis B virus (HBV Pol 455) and then incubated with a CTL cell line that responds to the HBV Pol 455 epitope/HLA-A2.1 complex by producing IFNγ. The capacity of Progenipoietin™-derived splenic DC to present the HBV Pol 455 epitope was greater than that of two positive control populations: GM-CSF and IL-4 expanded DC cultures, or purified splenic B cells. A left shift in the response curve for Progenipoietin™-derived spleen cells versus the other antigen presenting cells revealed that these Progenipoietin™-derived cells required less epitope to stimulate maximal IFNγ release by the responder cell line.

The ability of *ex vivo* peptide-pulsed DC to stimulate CTL responses *in vivo* was also evaluated using the HLA-A2.1 transgenic mouse model. DC derived from Progenipoietin™-treated animals or control DC derived from bone marrow cells after expansion with GM-CSF and IL-4 were pulsed *ex vivo* with the HBV Pol 455 CTL epitope, washed and injected (IV) into such mice. At seven days post immunization, spleens were removed and splenocytes containing DC and CTL were restimulated twice *in vitro* in the presence of the HBV Pol 455 peptide. The CTL activity of three independent cultures of restimulated spleen cell cultures was assessed by measuring the ability of the CTL to lyse ^{51}Cr-labeled target cells pulsed with or without peptide. Vigorous CTL responses were generated in animals immunized with the epitope-pulsed Progenipoietin™ derived DC as well as epitope-pulsed GM-CSF/IL-4 DC. In contrast, animals that were immunized with mock-pulsed Progenipoietin™-generated DC (no peptide) exhibited no evidence of CTL induction.

These data confirm that DC derived from Progenipoietin™ treated mice can be pulsed *ex vivo* with epitope and used to induce specific CTL responses *in vivo*. Thus, these data support the principle that Progenipoietin™-derived DC promote CTL responses in a model that manifests human MHC Class I molecules.

In vivo pharmacology studies in mice have demonstrated no apparent toxicity of reinfusion of pulsed autologous DC into animals.

Ex vivo activation of CTL/HTL responses

Alternatively, *ex vivo* CTL or HTL responses to a particular tumor-associated antigen can be induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of antigen-presenting cells (APC), such as dendritic cells, and the appropriate immunogenic peptides. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cells, *i.e.*, tumor cells.

Example 22. Alternative Method of Identifying Motif-Bearing Peptides

Another way of identifying motif-bearing peptides is to elute them from cells bearing defined MHC molecules. For example, EBV transformed B cell lines used for tissue typing, have been extensively characterized to determine which HLA molecules they express. In certain cases these cells express only a single type of HLA molecule. These cells can then be infected with a pathogenic organism or transfected with nucleic acids that express the tumor antigen of interest. Thereafter, peptides produced by endogenous antigen processing of peptides produced consequent to infection (or as a result of transfection) will bind to HLA molecules within the cell and be transported and displayed on the cell surface.

The peptides are then eluted from the HLA molecules by exposure to mild acid conditions and their amino acid sequence determined, e.g., by mass spectral analysis (*e.g.*, Kubo *et al.*, *J. Immunol.* 152:3913, 1994). Because, as disclosed herein, the majority of peptides that bind a particular HLA molecule are motif-bearing, this is an alternative modality for obtaining the motif-bearing peptides correlated with the particular HLA molecule expressed on the cell.

Alternatively, cell lines that do not express any endogenous HLA molecules can be transfected with an expression construct encoding a single HLA allele. These cells may then be used as described, *i.e.*, they may be infected with a pathogenic organism or transfected with nucleic acid encoding an antigen of interest to isolate peptides corresponding to the pathogen or antigen of interest that have been presented on the cell surface. Peptides obtained from such an analysis will bear motif(s) that correspond to binding to the single HLA allele that is expressed in the cell.

As appreciated by one in the art, one can perform a similar analysis on a cell bearing more than one HLA allele and subsequently determine peptides specific for each HLA allele expressed. Moreover, one of skill would also recognize that means other than infection or transfection, such as loading with a protein antigen, can be used to provide a source of antigen to the cell.

The above examples are provided to illustrate the invention but not to limit its scope. For example, the human terminology for the Major Histocompatibility Complex, namely HLA, is used throughout this document. It is to be appreciated that these principles can be extended to other species as well. Thus, other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent application cited herein are hereby incorporated by reference for all purposes.

TABLE I

SUPERMOTIFS	POSITION 2 (Primary Anchor)	POSITION 3 (Primary Anchor)	POSITION C Terminus (Primary Anchor)
A1	**T, I,** *L, V, M, S*		**F, W, Y**
A2	**L, I, V, M,** *A, T, Q*		**I, V,** *M, A, T, L*
A3	**V, S, M, A,** *T, L, I*		**R,K**
A24	**Y, F,** *W, I, V, L, M, T*		**F, I,** *Y, W, L, M*
B7	**P**		**V, I, L, F,** *M, W, Y, A*
B27	**R, H, K**		**F, Y, L,** *W, M, I, V, A*
B44	**E,** *D*		**F, W, L, I, M, V, A**
B58	**A, T, S**		**F, W, Y,** *L, I, V, M, A*
B62	**Q, L,** *I, V, M, P*		**F, W, Y,** *M, I, V, L, A*
MOTIFS			
A1	**T, S, M**		**Y**
A1		**D, E,** *A, S*	**Y**
A2.1	**L, M,** *V, Q, I, A, T*		**V,** *L, I, M, A, T*
A3	**L, M, V, I, S, A, T, F,** *C, G, D*		**K, Y, R,** *H, F, A*
A11	**V, T, M, L, I, S, A, G, N,** *C, D, F*		**K,** *R, Y, H*
A24	**Y, F, W,** *M*		**F, L, I, W**
A*3101	**M, V, T,** *A ,L, I, S*		**R,** *K*
A*3301	**M, V, A, L, F,** *I, S, T*		**R, K**
A*6801	**A, V, T,** *M, S, L, I*		**R, K**
B*0702	**P**		**L, M, F,** *W, Y, A, I, V*
B*3501	**P**		**L, M, F, W, Y,** *I, V, A*
B51	**P**		**L, I, V, F,** *W, Y, A, M*
B*5301	**P**		**I, M, F, W, Y,** *A, L, V*
B*5401	**P**		**A, T, I, V,** *L, M, F, W, Y*

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE Ia

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	**T, I,** *L, V, M, S*		**F, W, Y**
A2	**V,** *Q, A, T*		**I, V,** *L, M, A, T*
A3	**V, S, M, A,** *T, L, I*		**R, K**
A24	**Y, F,** *W, I, V, L, M, T*		**F, I,** *Y, W, L, M*
B7	**P**		**V, I, L, F,** *M, W, Y, A*
B27	**R, H, K**		**F, Y, L,** *W, M, I, V, A*
B58	**A, T, S**		**F, W, Y,** *L, I, V, M, A*
B62	**Q, L,** *I, V, M, P*		**F, W, Y,** *M, I, V, L, A*
MOTIFS			
A1	**T, S, M**		**Y**
A1		**D, E,***A, S*	**Y**
A2.1	*V, Q, A, T**		**V,** *L, I, M, A, T*
A3.2	**L, M, V, I, S, A, T, F,** *C, G, D*		**K, Y, R,** *H, F, A*
A11	**V, T, M, L, I, S, A, G, N,** *C, D, F*		**K,** *R, H, Y*
A24	**Y ,F, W**		**F, L, I, W**

*If 2 is V, or Q, the C-term is not L

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

		POSITION								
		1	2	3	4	5	6	7	8	C-terminus
SUPERMOTIFS										
A1			1° Anchor T,I,*L,V,M,S*							1° Anchor F,W,Y
A2			1° Anchor L,I,V,M,*A, T,Q*							1° Anchor L,I,V,M,A,T
A3	preferred		1° Anchor V,S,M,A,*T, L,I*	Y,F,W, (4/5)			Y,F,W, (3/5)	Y,F,W, (4/5)	P, (4/5)	1°Anchor R,K
	deleterious	D,E (3/5); P, (5/5)		D,E, (4/5)						
A24			1° Anchor Y,F,*W,I,V, L,M,T*							1° Anchor F,I,*Y,W,L,M*
B7	preferred	F,W,Y (5/5) L,I,V,M, (3/5)	1°Anchor P	F,W,Y (4/5)					F,W,Y, (3/5)	1°Anchor V,I,L,F,*M,W,Y,A*
	deleterious	D,E (3/5); P(5/5); G(4/5); A(3/5); Q,N, (3/5)				D,E, (3/5)	G, (4/5)	Q,N, (4/5)	D,E, (4/5)	
B27			1° Anchor R,H,K							1° Anchor F,Y,L,*W,M,V,A*
B44			1° Anchor E,*D*							1° Anchor F,W,Y,L,I,M,V,A
B58			1° Anchor A,T,S							1° Anchor F,W,Y,*L,I,V,M,A*
B62			1° Anchor Q,L,*I,V,M, P*							1° Anchor F,W,Y,*M,I,V,L,A*

		POSITION								
		1	2	3	4	5	6	7	8	C-terminus
MOTIFS										
A1 9-mer	preferred	G,F,Y,W,	1°Anchor S,T,M,	D,E,A,	Y,F,W,		P,	D,E,Q,N,	Y,F,W,	1°Anchor Y
	deleterious	D,E,		R,H,K,L,I,V M,P,	A,	G,	A,			
A1 9-mer	preferred	G,R,H,K	A,S,T,C,L,I V,M,	1°Anchor D,E,*A,S*	G,S,T,C,		A,S,T,C,	L,I,V,M,	D,E,	1°Anchor Y
	deleterious	A	R,H,K,D,E, P,Y,F,W,		D,E,	P,Q,N,	R,H,K,	P,G,	G,P,	

		POSITION								
		1	2	3	4	5	6	7	8	9 or C-terminus	C-terminus
A1 10-mer	peferred	Y,F,W,	1°Anchor S,T,M	D,E,A,Q,N,	A,	Y,F,W,Q,N,		P,A,S,T,C,	G,D,E,	P,	1°Anchor Y
	deleterious	G,P,		R,H,K,G,L,I V,M,	D,E,	R,H,K,	Q,N,A	R,H,K,Y,F, W,	R,H,K,	A	
A1 10-mer	preferred	Y,F,W,	S,T,C,L,I,V M,	1°Anchor D,E,*A,S*	A,	Y,F,W,		P,G,	G,	Y,F,W,	1°Anchor Y
	deleterious	R,H,K,	R,H,K,D,E, P,Y,F,W,			P,	G,		P,R,H,K,	Q,N,	
A2.1 9-mer	preferred	Y,F,W,	1°Anchor L,M,*I,V,Q, A,T*	Y,F,W,	S,T,C,	Y,F,W,		A,	P	1°Anchor V,*L,I,M,A,T*	
	deleterious	D,E,P,		D,E,R,K,H			R,K,H	D,E,R,K,H			
A2.1 10-mer	preferred	A,Y,F,W,	1°Anchor L,M,*I,V,Q, A,T*	L,V,I,M,	G,		G,		F,Y,W,L, V,I,M,		1°Anchor V,*L,I,M,A,T*
	deleterious	D,E,P,		D,E,	R,K,H,A,	P,		R,K,H,	D,E,R,K, H,	R,K,H,	

		POSITION									
		1	2	3	4	5	6	7	8	9 or C-terminus	C-terminus
A3	preferred	R,H,K,	1°Anchor L,M,V,I,S, A,T,F,*C,G D*	Y,F,W,	P,R,H,K,Y, F,W,	A,	Y,F,W,		P,	1°Anchor K,Y,R,*H,F,A*	
	deleterious	D,E,P,		D,E							
A11	preferred	A,	1°Anchor V,T,L,M,I, S,A,G,N,*C, D,F*	Y,F,W,	Y,FW,	A,	Y,F,W,	Y,FW,	P,	1°Anchor K,,*RY,H*	
	deleterious	D,E,P,						A	G,		
A24 9-mer	preferred	Y,F,W,R,H,K,	1°Anchor Y,F,W,*M*		S,T,C			Y,F,W,	Y,F,W,	1°Anchor F,L,I,W	
	deleterious	D,E,G,		D,E,	G,	Q,N,P,	D,E,R,H,K,	G,	A,Q,N,		
A24 10-mer	preferred		1°Anchor Y,F,W,*M*		P,	Y,F,W,P,		P,			1°Anchor F,L,I,W
	deleterious			G,D,E	Q,N	R,H,K	D,E	A	Q,N,	D,E,A,	
A3101	preferred	R,H,K,	1°Anchor M,V,T,*A,L, I,S*	Y,F,W,	P,		Y,F,W,	Y,F,W,	A,P,	1°Anchor R,*K*	
	deleterious	D,E,P,		D,E,		A,D,E,	D,E,	D,E,	D,E,		

		POSITION									
		1	2	3	4	5	6	7	8	9 or C-terminus	C-terminus
A3301	preferred		1°Anchor M,V,A,L,F, *I,S,T*	Y,F,W				A,Y,F,W		1°Anchor R,K	
	deleterious	G,P		D,E							
A6801	preferred	Y,F,W,S,T,C,	1°Anchor A,V,T,*M,S,* *L,I*			Y,F,W,L,I, V,M		Y,F,W,	P,	1°Anchor R,K	
	deleterious	G,P,		D,E,G,		R,H,K,			A,		
B0702	preferred	R,H,K,F,W,Y,	1°Anchor P	R,H,K,		R,H,K,	R,H,K,	R,H,K,	P,A,	1°Anchor L,M,F,*W,Y,A,* *I,V*	
	deleterious	D,E,Q,N,P,		D,E,P,	D,E,	D,E,	G,D,E,	Q,N,	D,E,		
B3501	preferred	F,W,Y,L,I,V,M,	1°Anchor P	F,W,Y,				F,W,Y,		1°Anchor L,M,F,W,Y,*I,* *V,A*	
	deleterious	A,G,P,				G,	G,				

		POSITION								
		1	2	3	4	5	6	7	8	9 or C-terminus	C-terminus
B51	preferred	L,I,V,M,F,W,Y,	1°Anchor P	F,W,Y,	S,T,C,	F,W,Y,		G,	F,W,Y,	1°Anchor L,I,V,F,*W, Y,A,M*	
	deleterious	A,G,P,D,E,R,H,K, S,T,C,				D,E,	G,	D,E,Q,N,	G,D,E,		
B5301	preferred	L,I,V,M,F,W,Y,	1°Anchor P	F,W,Y,	S,T,C,	F,W,Y,		L,I,V,M,F, W,Y,	F,W,Y,	1°Anchor I,M,F,W,Y, *A,L,V*	
	deleterious	A,G,P,Q,N,					G,	R,H,K,Q,N,	D,E,		
B5401	preferred	F,W,Y,	1°Anchor P	F,W,Y,L,I,V M,		L,I,V,M,		A,L,I,V,M,	F,W,Y,A,P,	1°Anchor A,T,I,V,*L, M,F,W,Y*	
	deleterious	G,P,Q,N,D,E,		G,D,E,S,T,C,		R,H,K,D,E,	D,E,	Q,N,D,G,E,	D,E,		

Italicized residues indicate less preferred or "tolerated" residues.
The information in Table II is specific for 9-mers unless otherwise specified.
Secondary anchor specificities are designated for each position independently.

Table III

MOTIFS		POSITION 1° anchor 1	2	3	4	5	1° anchor 6	7	8	9
DR4	preferred	F, M, Y, *L, I, V, W,*	M,	T,		I,	V, S, T, *C, P, A, L, I, M,*	M, H,		M, H
	deleterious				W,			R,		W, D, E
DR1	preferred	M, F, *L, I, V, W, Y,*			P, A, M, Q,		V, M, A, T, *S, P, L, I, C,*	M,		A, V, M
	deleterious		C	C, H	F, D	C, W, D		G, D, E,	D	
DR7	preferred	M, F, *L, I, V, W, Y,*	M,	W,	A,		I, V, M, S, A, *C, T, P, L,*	M,		I, V
	deleterious		C,		G,			G, R, D,	N	G
DR Supermotif		M, F, *L, I, V, W, Y,*					V, M, S, T, A, *C, P, L, I,*			

DR3 MOTIFS	1° anchor 1	2	3	1° anchor 4	5	1° anchor 6
motif a preferred	L, I, V, M, F, Y,			D		
motif b preferred	L, I, V, M, F, A, Y,			D, N, Q, E, S, T		K, R, H

Italicized residues indicate less preferred or "tolerated" residues. Secondary anchor specificities are designated for each position independently.

Table IV: HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE (SEQ ID NO:)	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	25
A*0201	941.01	FLPSDYFPSV	5.0
A*0202	941.01	FLPSDYFPSV	4.3
A*0203	941.01	FLPSDYFPSV	10
A*0205	941.01	FLPSDYFPSV	4.3
A*0206	941.01	FLPSDYFPSV	3.7
A*0207	941.01	FLPSDYFPSV	23
A*6802	1072.34	YVIKVSARV	8.0
A*0301	941.12	KVFPYALINK	11
A*1101	940.06	AVDLYHFLK	6.0
A*3101	941.12	KVFPYALINK	18
A*3301	1083.02	STLPETYVVRR	29
A*6801	941.12	KVFPYALINK	8.0
A*2402	979.02	AYIDNYNKF	12
B*0702	1075.23	APRTLVYLL	5.5
B*3501	1021.05	FPFKYAAAF	7.2
B51	1021.05	FPFKYAAAF	5.5
B*5301	1021.05	FPFKYAAAF	9.3
B*5401	1021.05	FPFKYAAAF	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence (SEQ ID NO:)	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2β1	507.02	GRTQDENPVVHFFKNIV TPRTPPP	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2β2	553.01	QYIKANSKFIGITE	20

Table VI

HLA-supertype	Allelle-specific HLA-supertype members: Verified[a]	Allelle-specific HLA-supertype members: Predicted[b]
A1	A*0101, A*2501, A*2601, A*2602, A*3201	A*0102, A*2604, A*3601, A*4301, A*8001
A2	A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, A*6901	A*0208, A*0210, A*0211, A*0212, A*0213
A3	A*0301, A*1101, A*3101, A*3301, A*6801	A*0302, A*1102, A*2603, A*3302, A*3303, A*3401, A*3402, A*6601, A*6602, A*7401
A24	A*2301, A*2402, A*3001	A*2403, A*2404, A*3002, A*3003
B7	B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, B*7801	B*1511, B*4201, B*5901
B27	B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, B*7301	B*2701, B*2707, B*2708, B*3802, B*3903, B*3904, B*3905, B*4801, B*4802, B*1510, B*1518, B*1503
B44	B*1801, B*1802, B*3701, B*4402, B*4403, B*4404, B*4001, B*4002, B*4006	B*4101, B*4501, B*4701, B*4901, B*5001
B58	B*5701, B*5702, B*5801, B*5802, B*1516, B*1517	
B62	B*1501, B*1502, B*1513, B*5201	B*1301, B*1302, B*1504, B*1505, B*1506, B*1507, B*1515, B*1520, B*1521, B*1512, B*1514, B*1510

a. Verified alleles include alleles whose specificity has been determined by pool sequencing analysis, peptide binding assays, or by analysis of the sequences of CTL epitopes.

b. Predicted alleles are alleles whose specificity is predicted on the basis of B and F pocket structure to overlap with the supertype specificity.

Table VII

Prostate A01 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0101	Seq. Id. No.
PAP	ALFPPEGVSIW	122	11		1
Kallikrein	ALGTTCYASGW	147	11		2
PSA	ALGTTCYASGW	143	11		3
Kallikrein	ALPEKPAVY	235	9		4
PSA	ALPERPSLY	231	9	0.0110	5
PSM	ALVLAGGF	25	8		6
PSM	ALVLAGGFF	25	9		7
PAP	AMTNLAALF	116	9		8
PAP	ASCHLTELY	311	9	0.7700	9
PAP	ASCHLTELYF	311	10		10
PSM	ASGRARYTKNW	531	11		11
PSM	ASKFSERLQDF	643	11		12
PAP	ASLSLGFLF	12	9		13
PSM	ASWDAEEF	419	8		14
PSM	ATARRPRW	13	8		15
PSM	AVATARRPRW	11	10		16
PSM	AVVHEIVRSF	393	10		17
Kallikrein	AVYTKVVHY	241	9		18
Kallikrein	CLKKNSQVW	66	9		19
PSM	CSGKIVIARY	196	10	0.0160	20
PAP	CSPSCPLERF	347	10		21
PSM	DIVPPFSAF	156	9		22
PAP	DLFGIWSKVY	201	10		23
PSA	DMSLLKNRF	98	9		24
PSM	DSLFSAVKNF	630	10		25
PSM	DSSIEGNY	453	8		26
PSM	DSVELAHY	106	8		27
PAP	DVYNGLLPPY	301	10		28
PSM	EIFNTSLF	137	8		29
PSM	ELAHYDVLLSY	109	11		30
PSM	ELANSIVLPF	586	10		31
PAP	ELGEYIRKRY	80	10		32
PSM	ELKAENIKKF	64	10		33
PAP	ELKFVTLVF	34	9		34
PSM	ELKSPDEGF	480	9		35
PAP	ELSELSLLSLY	237	11		36
PAP	ELSLLSLY	240	8		37
PSM	ELVEKFYDPMF	560	11		38
PAP	ELVGPVIPQDW	358	11		39
PAP	ELYFEKGEY	317	9		40
PAP	ELYFEKGEYF	317	10		41
PSM	EMKTYSVSF	621	9		42
PAP	ESETLKSEEF	168	10		43
PSM	ESFPGIYDALF	703	11		44
PSM	ESKVDPSKAW	716	10		45
PAP	ESSWPQGF	60	8		46

Table VII

Prostate A01 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0101	Seq. Id. No.
PAP	ESVHNFTLPSW	216	11		47
PAP	ESYKHEQVY	95	9	0.0980	48
PAP	ETLKSEEF	170	8		49
PSM	ETNKFSGY	542	8		50
PSM	ETNKFSGYPLY	542	11		51
PSM	ETYELVEKF	557	9		52
PSM	ETYELVEKFY	557	10	0.0260	53
PSM	EVKRQIYVAAF	727	11		54
PAP	FLFLLFFW	18	8		55
PSM	FLLGFLFGW	33	9		56
PSM	FLLGFLFGWF	33	10		57
PSA	FLTLSVTW	3	8		58
Kallikrein	FMLCAGLW	195	8		59
PSA	FMLCAGRW	191	8		60
PSM	FSERLQDF	646	8		61
PSM	FSGYPLYHSVY	546	11		62
PSM	FTEHASKF	639	8		63
PSM	GIASGRARY	529	9	0.0025	64
PAP	GIWSKVYDPLY	204	11		65
PSM	GLDSVELAHY	104	10	0.4800	66
PAP	GLHGQDLF	196	8		67
PAP	GLHGQDLFGIW	196	11		68
PSM	GLLGSTEW	427	8		69
PSM	GLPDRPFY	680	8		70
PAP	GLQMALDVY	295	9		71
PAP	GMEQHYELGEY	74	11		72
PSM	GMPEGDLVY	168	9	0.0001	73
PSM	GSAPPDSSW	311	9		74
PSM	GSGNDFEVF	516	9		75
PSM	GSGNDFEVFF	516	10		76
Kallikrein	GSIEPEEF	158	8		77
PSA	GSIEPEEF	154	8		78
PSM	GTLKKEGW	403	8		79
Kallikrein	GTTCYASGW	149	9		80
PSA	GTTCYASGW	145	9		81
PSM	GVILYSDPADY	224	11		82
PSM	GVKSYPDGW	238	9		83
Kallikrein	GVLQGITSW	221	9		84
PSA	GVLQGITSW	217	9		85
Kallikrein	GVLVHPQW	52	8		86
PSA	GVLVHPQW	48	8		87
PAP	GVSIWNPILLW	128	11		88
PSM	HLAGTEQNF	82	9		89
PAP	HMKRATQIPSY	270	11		90
Kallikrein	HSFPHPLY	94	8	0.0260	91
PSA	HSFPHPLY	90	8	0.0260	92

Prostate A01 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0101	Seq. Id. No.
Kallikrein	HSQPWQVAVY	34	10		93
PSM	HSTNEVTRIY	347	10	0.0048	94
PSM	HNEDGNEIF	130	10		95
PSM	ILFASWDAEEF	416	11		96
PSM	ILGGHRDSW	373	9		97
PSM	ILGGHRDSWVF	373	11		98
PSA	ILLGRHSLF	69	9		99
PSA	ILSRIVGGW	17	9		100
PSM	ILYSDPADY	226	9		101
PSM	ILYSDPADYF	226	10		102
PSM	ISKLGSGNDF	512	10		103
PSM	ITPKHNMKAF	52	10		104
PSM	IVIARYGKVF	200	10		105
PSM	IVLPFDCRDY	591	10		106
PSM	IVPPFSAF	157	8		107
PSM	KIVIARYGKVF	199	11		108
PSM	KLGSGNDF	514	8		109
PSM	KLGSGNDFEVF	514	11		110
PAP	KLSGLHGQDLF	193	11		111
PSM	KTYSVSFDSLF	623	11		112
PSM	KVDPSKAW	718	8		113
PSM	KVPYNVGPGF	324	10		114
Kallikrein	KVVHYRKW	245	8		115
PSA	KVVHYRKW	241	8		116
PSA	LILSRIVGGW	16	10		117
Kallikrein	LIQSRIVGGW	20	10		118
PSM	LLGFLFGW	34	8		119
PSM	LLGFLFGWF	34	9		120
PSA	LLGRHSLF	70	8		121
PSM	LLQERGVAY	441	9		122
Kallikrein	LLSNDMCARAY	178	11		123
PSM	LMFLERAF	668	8		124
PAP	LSEDQLLY	148	8		125
PAP	LSEDQLLYLPF	148	11		126
PAP	LSELSLLSLY	238	10	12.0000	127
PAP	LSGLHGQDLF	194	10		128
PAP	LSLGFLFLLF	14	10		129
PAP	LSLGFLFLLFF	14	11		130
Kallikrein	LSNDMCARAY	179	10		131
PSA	LSRIVGGW	18	8		132
PSM	LSYPNKTHPNY	117	11		133
PAP	LTELYFEKGEY	315	11		134
PSM	LTPGYPANEY	268	10	0.0082	135
PAP	LTQLGMEQHY	70	10	0.6200	136
PSM	LVEKFYDPMF	561	10		137
PAP	LVGPVIPQDW	359	10		138

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Prostate A01 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0101	Seq. Id. No.
PSM	LVLAGGFF	26	8		139
PSM	MMNDQLMF	663	8		140
PAP	MSAMTNLAALF	114	11		141
PSA	MSLLKNRF	99	8		142
PAP	MTNLAALF	117	8		143
PSM	NIKKFLYNF	69	9		144
PSM	NITPKHNMKAF	51	11		145
PSM	NVGPGFTGNF	328	10		146
PSM	NVSDIVPPF	153	9		147
PAP	PIKESSWPQGF	57	11		148
PSM	PLGLPDRPF	678	9		149
PSM	PLGLPDRPFY	678	10		150
PSA	PLILSRIVGGW	15	11		151
Kallikrein	PLIQSRIVGGW	19	11		152
PAP	PLSEDQLLY	147	9	1.2000	153
PSM	PLTPGYPANEY	267	11		154
PAP	PLYCESVHNF	212	10		155
PSM	PLYHSVYETY	550	10		156
PAP	PSCPLERF	349	8		157
PSM	PSIPVHPIGY	290	10		158
PSM	PSIPVHPIGYY	290	11		159
PSA	PSLYTKVVHY	236	10	0.0010	160
PAP	PSYKKLIMY	278	9	0.0031	161
PAP	PTDPIKESSW	54	10		162
PSM	PVHPIGYY	293	8		163
Kallikrein	PVSHSFPHPLY	91	11		164
PAP	QIPSYKKLIMY	276	11		165
PSM	QIQSQWKEF	95	9		166
PSM	QLAGAKGVILY	218	11		167
PSM	QLAKQIQSQW	91	10		168
PAP	QLGMEQHY	72	8		169
PSM	QLMFLERAF	667	9		170
PAP	QLTQLGMEQHY	69	11		171
Kallikrein	QSRIVGGW	22	8		172
Kallikrein	QVAVYSHGW	39	9		173
PSA	QVFQVSHSF	84	9		174
PSA	QVHPQKVTKF	182	10		175
PSM	QVRGGMVF	578	8		176
PSA	QVSHSFPHPLY	87	11		177
Kallikrein	QVWLGRHNLF	72	10		178
PSM	RISKLGSGNDF	511	11		179
PSM	RLGIASGRARY	527	11		180
PAP	RLHPYKDF	180	8		181
PSM	RLLQERGVAY	440	10		182
PSM	RMMNDQLMF	662	9		183
PSM	RSFGTLKKEGW	400	11		184

Table VI

Prostate A01 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0101	Seq. Id. No.
PAP	RSVLAKELKF	28	10		185
PSM	RTILFASW	414	8		186
PSM	RVDCTPLMY	463	9	11.0000	187
Kallikrein	RVPVSHSF	89	8		188
PSM	SHNEDGNEIF	129	11		189
PSM	SIPVHPIGY	291	9		190
PSM	SIPVHPIGYY	291	10		191
PSM	SIVLPFDCRDY	590	11		192
PAP	SIWNPILLW	130	9		193
PSM	SLFEPPPPGY	142	10		194
PSM	SLFSAVKNF	631	9		195
PAP	SLGFLFLLF	15	9		196
PAP	SLGFLFLLFF	15	10		197
PAP	SLGFLFLLFFW	15	11		198
PAP	SLSLGFLF	13	8		199
PAP	SLSLGFLFLLF	13	11		200
PSA	SLYTKVVHY	237	9	0.0017	201
PSM	SMKHPQEMKTY	615	11		202
PSM	SSHNKYAGESF	695	11		203
PSM	SSWRGSLKVPY	317	11		204
PSM	STNEVTRIY	348	9	0.0430	205
PAP	SVHNFTLPSW	217	10		206
PSA	SVILLGRHSLF	67	11		207
PAP	SVLAKELKF	29	9		208
PSM	SVSFDSLF	626	8		209
PSM	TLRGAVEPDRY	361	11		210
PSM	TLRVDCTPLMY	461	11		211
PSM	TSLFEPPPPGY	141	11		212
Kallikrein	TTCYASGW	150	8		213
PSA	TTCYASGW	146	8		214
PSM	TVAQVRGGMVF	575	11		215
PAP	TVPLSEDQLLY	145	11		216
PSM	VIARYGKVF	201	9		217
PSM	VILGGHRDSW	372	10		218
PSA	VILLGRHSLF	68	10		219
PSM	VILYSDPADY	225	10		220
PSM	VILYSDPADYF	225	11		221
PSM	VIYAPSSHNKY	690	11		222
PSM	VLAGGFFLLGF	27	11		223
PAP	VLAKELKF	30	8		224
PSM	VLPFDCRDY	592	9		225
Kallikrein	VLQGITSW	222	8		226
PSA	VLQGITSW	218	8		227
PSM	VLRKYADKIY	603	10		228
PSM	VLRMMNDQLMF	660	11		229
PSM	VSDIVPPF	154	8		230

Table VII

Prostate A01 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0101	Seq. Id. No.
PSM	VSDIVPPFSAF	154	11		231
PAP	VSGLQMALDVY	293	11		232
Kallikrein	VSHSFPHPLY	92	10	0.1500	233
PSA	VSHSFPHPLY	88	10	0.1500	234
PAP	VSIWNPILLW	129	10		235
Kallikrein	VTEFMLCAGLW	192	11		236
PSA	VTKFMLCAGRW	188	11		237
PSA	VVFLTLSVTW	1	10		238
PSM	VVHEIVRSF	394	9		239
PSM	VVLRKYADKIY	602	11		240
Kallikrein	WLGRHNLF	74	8		241
PAP	WSKVYDPLY	206	9	0.0046	242
PSM	WTKKSPSPEF	497	10		243
PAP	YIRKRYRKF	84	9		244
PAP	YLPFRNCPRF	155	10		245
PSM	YSDPADYF	228	8		246
Kallikrein	YSEKVTEF	188	8		247
PSM	YSVSFDSLF	625	9		248
PSM	YTKNWETNKF	537	10		249
Kallikrein	YTKVVHYRKW	243	10		250
PSA	YTKVVHYRKW	239	10		251
PSM	YVILGGHRDSW	371	11		252
PSM	YVNYARTEDF	176	10		253
PSM	YVNYARTEDFF	176	11		254

Table VIII

Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PSM	AAAETLSEV	741	9	0.0002					255
PSM	AAAETLSEVA	741	10						256
PSM	AAETLSEV	742	8						257
PSM	AAETLSEVA	742	9						258
PSM	AAFTVQAA	735	8						259
PSM	AAFTVQAAA	735	9						260
PSM	AAFTVQAAAET	735	11						261
PSA	AAHCIRNKSV	59	10	0.0002					262
PSA	AAHCIRNKSVI	59	11	0.0010	0.0100	0.0140	0.0004	0.0018	263
Kallikrein	AAHCLKKNSQV	63	11	0.0003	0.0006	0.0450	0.0001	0.0004	264
PAP	AALFPPEGV	121	9	0.0002					265
PAP	AALFPPEGVSI	121	11						266
PSA	AAPLILSRI	13	9	0.0002					267
PSA	AAPLILSRIV	13	10	0.0002					268
PAP	AAPLLLARA	3	9						269
PAP	AAPLLLARAA	3	10						270
PAP	AASLSLGFL	11	9	0.0002					271
PAP	AASLSLGFLFL	11	11						272
PSM	AAVVHEIV	392	8						273
PAP	ALDVYNGL	299	8						274
PAP	ALDVYNGLL	299	9	0.0520					275
PSM	ALFDIESKV	711	9	0.0590	6.0000	7.2000	0.0250	0.0009	276
PAP	ALFPPEGV	122	8						277
PAP	ALFPPEGVSI	122	10	0.0044					278
Kallikrein	ALGTTCYA	147	8	0.0230					279
PSA	ALGTTCYA	143	8	0.0230					280
Kallikrein	ALPEKPAV	235	8	0.0009	0.0200	0.0510	0.0001	-0.0001	281
Kallikrein	ALPEKPAVYT	235	10	0.0003	0.0050	0.0028	0.0005	-0.0001	282
PSA	ALPERPSL	231	8	0.0002					283
PSA	ALPERPSLYT	231	10	0.0008					284
Kallikrein	ALSVGCTGA	9	9	0.0410	0.0038	0.1100	0.0066	-0.0001	285
Kallikrein	ALSVGCTGAV	9	10	0.0180	0.2600	0.4000	0.0051	0.0012	286
PSM	ALVLAGGFFL	25	10	0.0150					287
PSM	ALVLAGGFFLL	25	11						288
PAP	AMTNLAAL	116	8						289
PSM	AQKLLEKM	302	8						290
PSM	AQLAGAKGV	217	9						291
PSM	AQLAGAKGVI	217	10						292
PSM	AQLAGAKGVIL	217	11						293
PSA	AQVHPQKV	181	8						294
PSA	AQVHPQKVT	181	9	0.0002					295
PSM	AQVRGGMV	577	8						296
PSM	AQVRGGMVFEL	577	11						297
PSM	ATARRPRWL	13	9	0.0002					298
PSM	ATARRPRWLCA	13	11						299
PAP	ATEDTMTKL	227	9	0.0002					300

Table VIII

Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PAP	ATLGKLSGL	189	9	0.0005					301
PSM	ATNITPKHNM	49	10						302
PAP	ATQIPSYKKL	274	10	0.0002					303
PAP	ATQIPSYKKLI	274	11						304
PSM	AVATARRPRWL	11	11						305
PSA	AVCGGVLV	44	8	0.0003					306
PSM	AVEPDRYV	365	8						307
PSM	AVEPDRYVI	365	9	0.0001					308
PSM	AVEPDRYVIL	365	10	0.0002					309
PSM	AVGLPSIPV	286	9	0.0042					310
PSM	AVKNFTEI	635	8						311
PSM	AVKNFTEIA	635	9						312
PSA	AVKVMDLPT	131	9	0.0001					313
Kallikrein	AVPLIQSRI	17	9	0.0001	0.0026	0.0013	0.0020	0.0610	314
Kallikrein	AVPLIQSRIV	17	10	0.0014	0.0510	0.0490	0.0035	0.0058	315
PSM	AVVLRKYA	601	8						316
PSM	AVVLRKYADKI	601	11						317
Kallikrein	AVYSHGWA	41	8	-0.0001	0.0005	0.0011	0.0004	0.0003	318
PSM	CAGALVLA	22	8						319
Kallikrein	CAGLWTGGKDT	198	11	0.0001	0.0003	0.0027	-0.0001	-0.0002	320
PSA	CAGRWTGGKST	194	11	0.0013	0.0370	0.0250	0.0002	0.0081	321
Kallikrein	CALPEKPA	234	8	-0.0001	-0.0001	-0.0001	-0.0001	-0.0001	322
Kallikrein	CALPEKPAV	234	9	0.0002	0.0013	0.1100	0.0004	0.0001	323
Kallikrein	CALPEKPAVYT	234	11	0.0008	0.0033	0.0120	0.1700	-0.0002	324
PSA	CALPERPSL	230	9	0.0001					325
PSA	CALPERPSLYT	230	11	0.0008	0.0130	0.0071	0.0016	0.0023	326
PSA	CAQVHPQKV	180	9	0.0002					327
PSA	CAQVHPQKVT	180	10	0.0001					328
Kallikrein	CARAYSEKV	184	9	-0.0001	0.0006	0.0025	0.0002	0.0012	329
Kallikrein	CARAYSEKVT	184	10	0.0074	0.0710	0.0200	0.0030	0.0071	330
PSA	CIRNKSVI	62	8	0.0001					331
PSA	CIRNKSVIL	62	9	0.0003					332
PSA	CIRNKSVILL	62	10	0.0001					333
Kallikrein	CLKKNSQV	66	8	0.0001	0.0006	0.0006	-0.0001	-0.0001	334
Kallikrein	CLKKNSQVWL	66	10	0.0001	0.0220	0.0083	0.0002	-0.0001	335
PAP	CMTTNSHQGT	372	10	0.0002					336
Kallikrein	CTGAVPLI	14	8	0.0001	0.0001	0.0001	0.0012	0.0004	337
PSM	CTPLMYSL	466	8						338
PSM	CTPLMYSLV	466	9	0.0004					339
PSA	CVDLHVISNDV	169	11	0.0001					340
Kallikrein	CVSLHLLSNDM	173	11	0.0002	0.0031	0.0020	0.0009	0.0007	341
PSM	DAEEFGLL	422	8						342
PSM	DAEEFGLLGST	422	11						343
PSM	DALFDIESKV	710	10	0.0004					344
PSM	DAQKLLEKM	301	9						345
PSA	DAVKVMDL	130	8	-0.0001	0.0003	-0.0001	-0.0001	0.0001	346

Table VIII

Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PSA	DAVKVMDLPT	130	10	0.0001					347
PSM	DIESKVDPSKA	714	11						348
PSM	DIVPPFSA	156	8						349
PAP	DLFGIWSKV	201	9	0.0002					350
PSA	DLHVISNDV	171	9	0.0003					351
PSA	DLHVISNDVCA	171	11	0.0001					352
Kallikrein	DLMLLRLSEPA	120	11	0.0022					353
PSA	DLMLLRLSEPA	116	11	0.0022					354
PSA	DLPTQEPA	136	8	0.0001					355
PSA	DLPTQEPAL	136	9	0.0003					356
PSA	DLPTQEPALGT	136	11	0.0041	0.0180	0.0100	0.0001	0.0009	357
Kallikrein	DLVLSIAL	3	8	0.0001	-0.0002	-0.0001	-0.0001	0.0006	358
Kallikrein	DLVLSIALSV	3	10	0.0010	0.0180	0.0052	0.0230	0.0051	359
PSM	DLVYVNYA	173	8						360
PSM	DLVYVNYART	173	10	0.0004					361
Kallikrein	DMCARAYSEKV	182	11	0.0001	0.0018	0.0130	0.0001	0.0170	362
PSM	DMKINCSGKI	191	10	0.0001					363
PSM	DMKINCSGKIV	191	11						364
PSA	DMSLLKNRFL	98	10	0.0001					365
PSM	DQLMFLERA	666	9						366
PSM	DQLMFLERAFI	666	11						367
Kallikrein	DTCGGDSGGPL	207	11	0.0001	-0.0001	0.0005	-0.0001	0.0005	368
PAP	DTFPTDPI	51	8						369
Kallikrein	DTGQRVPV	85	8	-0.0001	0.0001	-0.0001	-0.0001	0.0002	370
PSA	DTGQVFQV	81	8	-0.0001	-0.0001	-0.0001	-0.0001	0.0016	371
PAP	DTMTKLREL	230	9	0.0002					372
PAP	DTTVSGLQM	290	9						373
PAP	DTTVSGLQMA	290	10						374
PAP	DTTVSGLQMAL	290	11						375
PSA	DVCAQVHPQKV	178	11	0.0001					376
PAP	DVDRTLMSA	108	9						377
PAP	DVDRTLMSAM	108	10						378
PAP	DVDRTLMSAMT	108	11						379
PSM	DVLLSYPNKT	114	10						380
Kallikrein	DVVKVLGL	134	8	-0.0001	-0.0001	-0.0001	-0.0001	0.0024	381
Kallikrein	DVVKVLGLPT	134	10	0.0012	0.0230	0.0460	0.0004	0.0017	382
PAP	DVYNGLLPPYA	301	11						383
PSM	EATNITPKHNM	48	11						384
PSM	EAVGLPSI	285	8						385
PSM	EAVGLPSIPV	285	10	0.0002					386
PSM	EIASKFSERL	641	10	0.0001					387
PAP	EILNHMKRA	266	9						388
PAP	EILNHMKRAT	266	10						389
PSM	EIVRSFGT	397	8						390
PSM	EIVRSFGTL	397	9	0.0002					391
PSM	ELAIHYDVL	109	8						392

Table VII

Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PSM	ELAIIYDVLL	109	9	0.0028					393
PSM	ELANSIVL	586	8						394
PSM	ELKAENIKKFL	64	11						395
PAP	ELKFVTLV	34	8						396
PAP	ELSELSLL	237	8						397
PAP	ELSELSLLSL	237	10	0.0008					398
PAP	ELSLLSLYGI	240	10	0.0002					399
PSA	ELTDAVKV	127	8	0.0001					400
PSA	ELTDAVKVM	127	9	0.0001					401
PSA	ELTDAVKVMDL	127	11	0.0001					402
PSM	ELVEKFYDPM	560	10	0.0001					403
PAP	ELYFEKGEYFV	317	11						404
PAP	EMYYRNET	328	8						405
PAP	EQIIYELGEYI	76	10						406
PSM	EQNFQLAKQI	87	10						407
PAP	EQVYIRST	100	8						408
PAP	EQVYIRSTDV	100	10						409
PSM	ETDSAVAT	7	8						410
PSM	ETDSAVATA	7	9						411
PSM	ETNKFSGYPL	542	10	0.0002					412
PAP	ETQIIEPYPL	334	9	0.0002					413
PAP	ETQIIEPYPLM	334	10						414
PAP	ETQIIEPYPLML	334	11						415
PSM	EVFFQRLGI	522	9	0.0002					416
PSM	EVFFQRLGIA	522	10						417
PSM	EVKRQIYV	727	8						418
PSM	EVKRQIYVA	727	9						419
PSM	EVKRQIYVAA	727	10						420
PSM	EVTRIYNV	351	8						421
PSM	EVTRIYNVI	351	9	0.0002					422
PSM	EVTRIYNVIGT	351	11						423
PAP	FAELVGPV	356	8						424
PAP	FAELVGPVI	356	9	0.0002					425
PSM	FASWDAEEFGL	418	11						426
PAP	FIATLGKL	187	8						427
PAP	FIATLGKLSGL	187	11						428
PSM	FIKSSNEA	42	8						429
PSM	FIKSSNEAT	42	9						430
PSM	FIKSSNEATNI	42	11						431
PSM	FLDELKAENI	61	10	0.0160					432
PSM	FLERAFIDPL	670	10	0.0014					433
PAP	FLFLLFFWL	18	9	0.0011					434
PAP	FLLFFWLDRSV	20	11						435
PSM	FLLGFLFGWFI	33	11						436
PAP	FLNESYKHEQV	92	11						437
Kallikrein	FLRPRSLQCV	165	10	0.0410	0.0940	1.1000	0.0068	0.0036	438

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Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PSA	FLTLSVTWI	3	9	0.0150					439
PSA	FLTLSVTWIGA	3	11	0.0160					440
PSA	FLTPKKLQCV	161	10	0.0310					441
PSM	FLYNFTQI	73	8						442
PSM	FLYNFTQIPHL	73	11						443
Kallikrein	FMLCAGLWT	195	9	0.0220	0.0019	0.0160	0.0170	0.0006	444
PSA	FMLCAGRWT	191	9	0.0059					445
PAP	FQELESET	164	8						446
PAP	FQELESETL	164	9						447
PSM	FQRLGIASGRA	525	11						448
PSA	FQVSHSFPHPL	86	11						449
PSM	FTGNFSTQKV	333	10	0.0001					450
PAP	FTLPSWAT	221	8						451
PAP	FTLPSWATEDT	221	11						452
PSM	FTQIPHLA	77	8						453
PSM	FTQIPHLAGT	77	10						454
PSM	FTVQAAAET	737	9						455
PSM	FTVQAAAETL	737	10	0.0001					456
PAP	FVEMYYRNET	326	10						457
PSA	GAAPLILSRI	12	10	0.0005					458
PSA	GAAPLILSRIV	12	11	0.1700	0.0220	0.0110	0.0006	0.0017	459
PSM	GAAVVHEI	391	8						460
PSM	GAAVVHEIV	391	9	0.0002					461
PSM	GALVLAGGFFL	24	11						462
PSM	GAVEPDRYV	364	9	0.0001					463
PSM	GAVEPDRYVI	364	10	0.0002					464
PSM	GAVEPDRYVIL	364	11						465
Kallikrein	GAVPLIQSRI	16	10	0.0017	0.0520	0.0380	0.0041	0.0057	466
Kallikrein	GAVPLIQSRIV	16	11	0.0001	0.0004	0.0004	0.0003	0.0003	467
PSM	GIAEAVGL	282	8						468
PSM	GIAEAVGLPSI	282	11						469
PSM	GIASGRARYT	529	10						470
PSM	GIDPQSGA	385	8						471
PSM	GIDPQSGAA	385	9						472
PSM	GIDPQSGAAV	385	10	0.0002					473
PSM	GIDPQSGAAVV	385	11						474
PAP	GIHKQKEKSRL	248	11						475
Kallikrein	GITSWGPEPCA	225	11	0.0009	0.0014	0.0230	0.0001	0.0004	476
PSA	GITSWGSEPCA	221	11	0.0001					477
PAP	GIWSKVYDPL	204	10	0.0002					478
PSM	GIYDALFDI	707	9	0.0210					479
PSM	GLDSVELA	104	8						480
PAP	GLHGQDLFGI	196	10	0.0340					481
PSM	GLLGSTEWA	427	9	0.0079					482
PAP	GLLPPYASCHL	305	11						483
PSM	GLPDRPFYRHV	680	11						484

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Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PSM	GLPSIPVHPI	288	10	0.0340	1.6000	4.7000	0.0015	0.0260	485
Kallikrein	GLPTQEPA	140	8	-0.0001	0.0003	-0.0001	-0.0001	-0.0001	486
Kallikrein	GLPTQEPAL	140	9	0.0002	0.0092	0.0013	0.0007	-0.0002	487
Kallikrein	GLPTQEPALGT	140	11	0.0003	0.0200	0.0450	0.0006	0.0020	488
PAP	GLQMALDV	295	8						489
Kallikrein	GLWTGGKDT	200	9	0.0002	0.0007	0.0015	-0.0001	-0.0002	490
PAP	GMEQIIYEL	74	8						491
PSM	GMPEGDLV	168	8						492
PSM	GMPEGDLVYV	168	10	0.0910	1.4000	1.4000	0.0230	0.0013	493
PSM	GMPRISKL	508	8						494
PSM	GMVFELANSI	582	10	0.0024					495
PSM	GMVFELANSIV	582	11						496
PAP	GQDLFGIWSKV	199	11						497
PAP	GQLTQLGM	68	8						498
PSM	GTEQNFQL	85	8						499
PSM	GTEQNFQLA	85	9						500
PSM	GVAYINADSSI	446	11						501
PSM	GVILYSDPA	224	9						502
PSM	GVKSYPDGWNL	238	11						503
Kallikrein	GVLVHPQWV	52	9	0.0003					504
PSA	GVLVHPQWV	48	9	0.0003					505
Kallikrein	GVLVHPQWVL	52	10	0.0004					506
PSA	GVLVHPQWVL	48	10	0.0004					507
Kallikrein	GVLVHPQWVLT	52	11	0.0002	0.0005	0.0005	0.0014	-0.0001	508
PSA	GVLVHPQWVLT	48	11	0.0002	0.0005	0.0005	0.0014	-0.0001	509
PAP	GVLVNEIL	261	8						510
PAP	GVLVNEILNIM	261	11						511
PSM	GVQRGNIL	252	8						512
PSM	GVQRGNILNL	252	10	0.0001					513
PAP	GVSIWNPI	128	8						514
PAP	GVSIWNPIL	128	9	0.0034					515
PAP	GVSIWNPILL	128	10	0.0016					516
PSM	HHISTNEV	345	8						517
PSM	HHISTNEVT	345	9						518
PSM	HHISTNEVTRI	345	11						519
PSM	HLAGTEQNFQL	82	11						520
Kallikrein	HLLSNDMCA	177	9	0.0020	0.0049	0.0005	0.0009	0.0003	521
Kallikrein	HLLSNDMCARA	177	11	0.0290	0.0520	0.1100	0.0088	0.0004	522
PSM	HLTVAQVRGGM	573	11						523
PAP	HMKRATQI	270	8						524
PAP	HQGTEDST	378	8						525
PAP	HTVPLSEDQL	144	10	0.0002					526
PAP	HTVPLSEDQLL	144	11						527
PSA	HVISNDVCA	173	9	0.0001					528
PSA	HVISNDVCAQV	173	11	0.0024					529
PSM	IAEAVGLPSI	283	10	0.0001					530

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Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
Kallikrein	IALSVGCT	8	8	0.0001	-0.0002	-0.0001	-0.0001	0.0003	531
Kallikrein	IALSVGCTGA	8	10	0.0013	0.0500	0.0180	0.0180	0.0005	532
Kallikrein	IALSVGCTGAV	8	11	0.0009	0.0032	0.0270	0.0100	0.0061	533
PSM	IASGRARYT	530	9						534
PSM	IASKFSERL	642	9	0.0001					535
PAP	IATLGKLSGL	188	10	0.0002					536
PSM	IINEDGNEI	130	9	0.0002					537
PSM	ILFASWDA	416	8						538
PSM	ILGGHRDSWV	373	10	0.0003					539
PSA	ILLGRHSL	69	8	0.0010					540
PAP	ILLWQPIPV	135	9	1.3000					541
PAP	ILLWQPIPVHT	135	11						542
PAP	ILNIIMKRA	267	8						543
PAP	ILNIIMKRAT	267	9	0.0001					544
PAP	ILNIIMKRATQI	267	11						545
PSM	ILNLNGAGDPL	258	11						546
PSM	ILYSDPADYFA	226	11						547
PAP	IMYSAIIDT	284	8						548
PAP	IMYSAIIDTT	284	9	0.0019					549
PAP	IMYSAIIDTTV	284	10	0.0610					550
PSM	IQSQWKEFGL	96	10						551
Kallikrein	ITDVVKVL	132	8	0.0001	0.0010	0.0001	-0.0001	0.0002	552
Kallikrein	ITDVVKVLGL	132	10	0.0003	0.0084	0.0088	0.0004	0.0005	553
PSM	ITPKHNMKA	52	9						554
PSM	ITPKHNMKAFL	52	11						555
Kallikrein	ITSWGPEPCA	226	10	0.0003	0.0100	0.0031	0.0005	0.0002	556
Kallikrein	ITSWGPEPCAL	226	11	0.0003	0.0150	0.0007	0.0013	0.0350	557
PSA	ITSWGSEPCA	222	10	0.0003	0.0036	0.0030	0.0001	0.0003	558
PSA	ITSWGSEPCAL	222	11	0.0010	0.0120	0.0096	0.0001	0.0003	559
PSM	IVIARYGKV	200	9	0.0001					560
PSM	IVLPFDCRDYA	591	11						561
PSM	IVLRMMNDQL	659	10	0.0004					562
PSM	IVLRMMNDQLM	659	11						563
PSM	IVRSFGTL	398	8						564
PSM	KAENIKKFL	66	9	0.0002					565
PSM	KAFLDELKA	59	9						566
PSM	KAWGEVKRQI	723	10	0.0001					567
PSM	KINCSGKI	193	8						568
PSM	KINCSGKIV	193	9	0.0002					569
PSM	KINCSGKIVI	193	10	0.0001					570
PSM	KINCSGKIVIA	193	11						571
Kallikrein	KITDVVKV	131	8	0.0004	0.0002	0.0017	0.0002	-0.0001	572
Kallikrein	KITDVVKVL	131	9	0.0047	0.0500	0.0420	0.0021	0.0002	573
Kallikrein	KITDVVKVLGL	131	11	0.0002	0.0053	0.1700	0.0011	0.0006	574
PSM	KIVIARYGKV	199	10	0.0002					575
PSM	KLERDMKI	187	8						576

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Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PSM	KLGSGNDFEV	514	10	0.0140					577
PAP	KLIMYSAHDT	282	10	0.0002					578
PAP	KLIMYSAHDTT	282	11						579
PSM	KLLEKMGGSA	304	10	0.0003					580
PSA	KLQCVDLHV	166	9	0.0190					581
PSA	KLQCVDLHVI	166	10	0.0370					582
PAP	KLRELSEL	234	8						583
PAP	KLRELSELSL	234	10	0.0040					584
PAP	KLRELSELSLL	234	11						585
PAP	KLSGLHGQDL	193	10	0.0026					586
PSM	KMHHHSTNEV	343	10	0.0042					587
PSM	KMHHHSTNEVT	343	11						588
PAP	KQKEKSRL	251	8						589
PSM	KTHPNYISI	122	9	0.0002					590
PSM	KTHPNYISII	122	10	0.0001					591
PSM	KTYSVSFDSL	623	10	0.0002					592
PSM	KVDPSKAWGEV	718	11						593
PSM	KVFRGNKV	207	8						594
PSM	KVFRGNKVKNA	207	11						595
PSM	KVKMHHHST	341	9						596
PSM	KVKNAQLA	213	8						597
PSM	KVKNAQLAGA	213	10						598
Kallikrein	KVLGLPTQEPA	137	11	0.0001	0.0004	0.0009	0.0012	0.0005	599
PSA	KVMDLPTQEPA	133	11	0.0014					600
PSM	KVPYNVGPGFT	324	11						601
Kallikrein	KVTEFMLCA	191	9	0.0035	0.0092	0.1900	0.1600	0.0004	602
Kallikrein	KVTEFMLCAGL	191	11	0.0010	0.0280	0.0280	0.0160	0.0036	603
PSA	KVTKFMLCA	187	9	0.0020					604
Kallikrein	KVVHYRKWI	245	9	0.0001					605
PSA	KVVHYRKWI	241	9	0.0001					606
PAP	KVYDPLYCESV	208	11						607
PAP	LAALFPPEGV	120	10	0.0017					608
PSM	LAGAKGVI	219	8						609
PSM	LAGAKGVIL	219	9	0.0002					610
PSM	LAGGFFLL	28	8						611
PSM	LAGGFFLLGFL	28	11						612
PSM	LAGTEQNFQL	83	10	0.0001					613
PSM	LAGTEQNFQLA	83	11						614
PSM	LAIIYDVLL	110	8						615
PAP	LAKELKFV	31	8						616
PAP	LAKELKFVT	31	9						617
PAP	LAKELKFVTL	31	10	0.0002					618
PAP	LAKELKFVTLV	31	11						619
PAP	LARAASLSL	8	9	0.0002					620
PAP	LIMYSAHDT	283	9						621
PAP	LIMYSAHDTT	283	10						622

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Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PAP	LIMYSAHDTTV	283	11						623
PAP	LLARAASL	7	8						624
PAP	LLARAASLSL	7	10	0.0061					625
PSM	LLEKMGGSA	305	9	0.0001					626
PAP	LLFFWLDRSV	21	10	0.6000					627
PAP	LLFFWLDRSVL	21	11						628
PSM	LLGFLFGWFI	34	10	0.0058					629
PSM	LLGSTEWA	428	8						630
PSM	LLHETDSA	4	8						631
PSM	LLHETDSAV	4	9	0.0180					632
PSM	LLHETDSAVA	4	10	0.0006					633
PSM	LLHETDSAVAT	4	11						634
PAP	LLLARAASL	6	9	0.0120					635
PAP	LLLARAASLSL	6	11						636
PAP	LLPPYASCHL	306	10	0.0017					637
PAP	LLPPYASCHLT	306	11						638
PSM	LLQERGVA	441	8						639
PSM	LLQERGVAYI	441	10	0.0280	0.7500	1.5000	0.0043	0.0006	640
Kallikrein	LLRLSEPA	123	8	0.0001					641
PSA	LLRLSEPA	119	8	0.0001					642
PSA	LLRLSEPAEL	119	10	0.0001					643
PSA	LLRLSEPAELT	119	11	0.0023	0.0140	0.0150	0.0002	0.0010	644
Kallikrein	LLRLSEPAKI	123	10	0.0030	0.0290	0.9200	0.0010	0.0008	645
Kallikrein	LLRLSEPAKIT	123	11	0.0002	0.0007	0.0180	-0.0001	-0.0001	646
Kallikrein	LLSNDMCA	178	8	0.0003	0.0073	0.0003	0.0021	-0.0001	647
Kallikrein	LLSNDMCARA	178	10	0.0030	0.0800	0.0280	0.0020	0.0042	648
PSM	LLSYPNKT	116	8						649
PAP	LLWQPIPV	136	8						650
PAP	LLWQPIPVIIT	136	10	0.0074					651
PAP	LLWQPIPVIITV	136	11						652
PSM	LMFLERAFI	668	9	0.0110					653
Kallikrein	LMLLRLSEPA	121	10	0.0018					654
PSA	LMLLRLSEPA	117	10	0.0018					655
PAP	LMSAMTNL	113	8						656
PAP	LMSAMTNLA	113	9	0.0071					657
PAP	LMSAMTNLAA	113	10	0.0037					658
PAP	LMSAMTNLAAL	113	11						659
PSM	LMYSLVHNL	469	9	0.0780	11.0000	4.8000	0.0340	0.0250	660
PSM	LMYSLVHNLT	469	10	0.0046					661
PSA	LQCVDLHV	167	8						662
PSA	LQCVDLHVI	167	9						663
Kallikrein	LQCVSLHL	171	8						664
Kallikrein	LQCVSLHLL	171	9						665
PSM	LQDFDKSNPI	650	10						666
PSM	LQDFDKSNPIV	650	11						667
PSM	LQERGVAYI	442	9						668

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Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PSM	LQERGVAYINA	442	11						669
PAP	LQGGVLVNEI	258	10						670
PAP	LQGGVLVNEIL	258	11						671
PAP	LQMALDVYNGL	296	11						672
PSA	LTDAVKVM	128	8	-0.0001	-0.0001	0.0002	-0.0001	0.0001	673
PSA	LTDAVKVMDL	128	10	0.0002					674
PSA	LTLSVTWI	4	8	0.0003	-0.0001	0.0006	0.0007	0.0001	675
PSA	LTLSVTWIGA	4	10	0.0018	0.0450	0.0820	0.0110	0.0910	676
PSA	LTLSVTWIGAA	4	11	0.0008	0.0014	0.0370	0.0025	0.0062	677
PSM	LTPGYPANEYA	268	11						678
PSA	LTPKKLQCV	162	9	0.0003					679
PSA	LTPKKLQCVDL	162	11	0.0007	0.0087	0.0074	0.0004	0.0021	680
PSM	LTVAQVRGGM	574	10						681
PSM	LTVAQVRGGMV	574	11						682
PSA	LVASRGRA	37	8	0.0001					683
PSA	LVASRGRAV	37	9	0.0003					684
Kallikrein	LVCNGVLQGI	217	10	0.0004					685
PSA	LVCNGVLQGI	213	10	0.0004					686
Kallikrein	LVCNGVLQGIT	217	11	0.0007	0.0034	0.0033	0.0049	0.0041	687
PSA	LVCNGVLQGIT	213	11	0.0007	0.0034	0.0033	0.0049	0.0041	688
PSM	LVEKFYDPM	561	9						689
PAP	LVFRHGDRSPI	40	11						690
PSM	LVHNETKEL	473	9	0.0001					691
Kallikrein	LVHPQWVL	54	8	0.0001					692
PSA	LVHPQWVL	50	8	0.0001					693
Kallikrein	LVHPQWVLT	54	9	0.0001					694
PSA	LVHPQWVLT	50	9	0.0001					695
Kallikrein	LVHPQWVLTA	54	10	0.0001					696
PSA	LVHPQWVLTA	50	10	0.0001					697
Kallikrein	LVHPQWVLTAA	54	11	0.0001					698
PSA	LVHPQWVLTAA	50	11	0.0001					699
PSM	LVLAGGFFL	26	9	0.0280	0.0030	0.0004	0.1100	0.0003	700
PSM	LVLAGGFFLL	26	10	0.0021					701
Kallikrein	LVLSIALSV	4	9	0.0020	0.0027	0.0085	0.0190	0.0002	702
PAP	LVNEILNHM	263	9						703
PSM	LVYVNYART	174	9						704
PAP	MALDVYNGL	298	9	0.0037					705
PAP	MALDVYNGLL	298	10	0.0010					706
Kallikrein	MLCAGLWT	196	8	0.0014	0.0020	0.0018	0.0001	0.0002	707
PSA	MLCAGRWT	192	8	0.0006	0.0012	0.0033	-0.0001	0.0001	708
Kallikrein	MLLRLSEPA	122	9	0.0610					709
PSA	MLLRLSEPA	118	9	0.0610					710
PSA	MLLRLSEPAEL	118	11	0.1400					711
Kallikrein	MLLRLSEPAKI	122	11	0.0044	0.0072	0.2100	0.0019	0.0007	712
PAP	MLPGCSPSCPL	343	11						713
PSM	MMNDQLMFL	663	9	0.4400	5.7000	5.8000	0.4900	0.0410	714

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Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PAP	MTKLRELSEL	232	10	0.0002					715
PAP	MTTNSHQGT	373	9						716
PSM	MVFELANSI	583	9	0.0170					717
PSM	MVFELANSIV	583	10	0.0140					718
PSM	MVFELANSIVL	583	11						719
PSM	NADSSIEGNYT	451	11						720
PSM	NAQLAGAKGV	216	10	0.0002					721
PSM	NAQLAGAKGVI	216	11						722
PSM	NIKKFLYNFT	69	10						723
PSM	NILNLNGA	257	8						724
PSM	NITPKHNM	51	8						725
PSM	NITPKHNMKA	51	10						726
PAP	NLAALFPPEGV	119	11						727
Kallikrein	NLFEPEDT	79	8	0.0002	0.0035	0.0004	-0.0001	0.0004	728
PSM	NLLHETDSA	3	9	0.0001					729
PSM	NLLHETDSAV	3	10	0.0027					730
PSM	NLLHETDSAVA	3	11						731
PSM	NLNGAGDPL	260	9	0.0007					732
PSM	NLNGAGDPLT	260	10	0.0002					733
PSM	NMKAFLDEL	57	9	0.0026					734
PSM	NMKAFLDELKA	57	11						735
Kallikrein	NMSLLKHQSL	102	10	0.0043	0.0260	0.0400	0.0058	0.0020	736
PSM	NVIGTLRGA	357	9						737
PSM	NVIGTLRGAV	357	10	0.0001					738
PSM	NVSDIVPPFSA	153	11						739
PSM	PADYFAPGV	231	9	0.0001					740
PSA	PAELTDAV	125	8	-0.0001	-0.0001	-0.0001	-0.0001	-0.0001	741
PSA	PAELTDAVKV	125	10	0.0002					742
PSA	PAELTDAVKVM	125	11	0.0003	0.0028	0.0008	-0.0001	-0.0001	743
Kallikrein	PAKITDVV	129	8	0.0001	0.0003	-0.0001	-0.0001	-0.0001	744
Kallikrein	PAKITDVVKV	129	10	0.0011	0.0100	0.0320	0.0006	0.0002	745
Kallikrein	PAKITDVVKVL	129	11	0.0002	0.0006	0.0017	-0.0001	0.0001	746
Kallikrein	PALGTTCYA	146	9	0.0083	0.0210	0.0270	0.0002	0.0035	747
PSA	PALGTTCYA	142	9	0.0083	0.0210	0.0270	0.0002	0.0035	748
PSM	PANEYAYRRGI	273	11						749
Kallikrein	PAVYTKVV	240	8	0.0001	-0.0001	-0.0001	-0.0001	-0.0001	750
PAP	PIDTFPTDPI	49	10	0.0002					751
PSM	PIGYYDAQKL	296	10	0.0001					752
PSM	PIGYYDAQKLL	296	11						753
PAP	PILLWQPI	134	8						754
PAP	PILLWQPIPV	134	10	0.0075					755
PAP	PIPVHTVPL	140	9	0.0002					756
PSM	PIVLRMMNDQL	658	11						757
PAP	PLERFAEL	352	8						758
PAP	PLERFAELV	352	9	0.0001					759
PSA	PLILSRIV	15	8	0.0001					760

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Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
Kallikrein	PLIQSRIV	19	8	0.0001	0.0002	-0.0001	-0.0001	-0.0001	761
PAP	PLLLARAA	5	8						762
PAP	PLLLARAASL	5	10	0.0004					763
PSM	PLMYSLVHNL	468	10	0.0008					764
PSM	PLMYSLVHNLT	468	11						765
PAP	PLSEDQLL	147	8						766
PAP	PLSEDQLLYL	147	10	0.0006					767
PSM	PLTPGYPA	267	8						768
Kallikrein	PLVCNGVL	216	8	0.0001					769
PSA	PLVCNGVL	212	8	0.0001					770
Kallikrein	PLVCNGVLQGI	216	11	0.0020					771
PSA	PLVCNGVLQGI	212	11	0.0020					772
PAP	PLYCESVHNFT	212	11						773
PSA	PLYDMSLL	95	8	0.0002					774
PSM	PLYHSVYET	550	9	0.0002					775
Kallikrein	PLYNMSLL	99	8	0.0002	0.0008	0.0002	-0.0001	-0.0001	776
PSM	PMFKYHLT	568	8						777
PSM	PMFKYHLTV	568	9	0.0042					778
PSM	PMFKYHLTVA	568	10	0.0005					779
PAP	PQDWSTECM	365	9						780
PAP	PQDWSTECMT	365	10						781
PAP	PQDWSTECMTT	365	11						782
PSM	PQEMKTYSV	619	9						783
PAP	PQGFGQLT	64	8						784
PAP	PQGFGQLTQL	64	10						785
PSM	PQGMPEGDL	166	9						786
PSM	PQGMPEGDLV	166	10						787
PSA	PQKVTKFM	185	8						788
PSA	PQKVTKFML	185	9						789
PSA	PQKVTKFMLCA	185	11						790
PSM	PQSGAAVV	388	8						791
PSM	PQSGAAVVHEI	388	11						792
Kallikrein	PQWVLTAA	57	8						793
PSA	PQWVLTAA	53	8						794
PSA	PQWVLTAAHCI	53	11						795
Kallikrein	PQWVLTAAHCL	57	11						796
Kallikrein	PTQEPALGT	142	9	0.0001					797
PSA	PTQEPALGT	138	9	0.0001					798
Kallikrein	PTQEPALGTT	142	10	0.0084	0.0220	0.0520	0.0037	0.0005	799
PSA	PTQEPALGTT	138	10	0.0084	0.0220	0.0520	0.0037	0.0005	800
PSM	PVHPIGYYDA	293	10						801
PAP	PVIPQDWST	362	9						802
Kallikrein	PVSHSFPHPL	91	10	0.0019	0.0099	0.0680	0.0022	0.0011	803
PSM	QAAAETLSEV	740	10	0.0006					804
PSM	QAAAETLSEVA	740	11						805
PSM	QIPHLAGT	79	8						806

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Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PAP	QIPSYKKL	276	8						807
PAP	QIPSYKKLI	276	9	0.0002					808
PAP	QIPSYKKLIM	276	10						809
PSM	QIQSQWKEFGL	95	11						810
PSM	QIYVAAFT	731	8						811
PSM	QIYVAAFTV	731	9	0.0026					812
PSM	QIYVAAFTVQA	731	11						813
PSM	QLAGAKGV	218	8						814
PSM	QLAGAKGVI	218	9	0.0001					815
PSM	QLAGAKGVIL	218	10	0.0006					816
PAP	QLGMEQHYEL	72	10	0.0003					817
PSM	QLMFLERA	667	8						818
PSM	QLMFLERAFI	667	10	0.0510	0.1200	0.1100	0.0003	0.2700	819
PAP	QMALDVYNGL	297	10	0.0002					820
PAP	QMALDVYNGLL	297	11						821
Kallikrein	QVAVYSHGWA	39	10	0.0004	0.0097	0.0200	0.0005	0.0252	822
PSA	QVHPQKVT	182	8	-0.0001	-0.0001	0.0001	-0.0001	-0.0001	823
PSA	QVHPQKVTKFM	182	11	0.0001					824
PSA	QVLVASRGRA	35	10	0.0001					825
PSA	QVLVASRGRAV	35	11	0.0001					826
PSM	QVRGGMVFEL	578	10	0.0001					827
PSM	QVRGGMVFELA	578	11						828
PSA	QVSHSFPHPL	87	10	0.0001					829
Kallikrein	QVWLGRHNL	72	9	0.0001	0.0021	0.0011	0.0025	0.0510	830
PAP	QVYIRSTDV	101	9	0.0002					831
PAP	RAAPLLLA	2	8						832
PAP	RAAPLLLARA	2	10						833
PAP	RAAPLLLARAA	2	11						834
PAP	RAASLSLGFL	10	10	0.0002					835
PSM	RAFIDPLGL	673	9	0.0001					836
PSM	RARYTKNWET	534	10						837
PAP	RATQIPSYKKL	273	11						838
PSA	RAVCGGVL	43	8	-0.0001	-0.0001	0.0003	-0.0001	-0.0001	839
PSA	RAVCGGVLV	43	9	0.0002					840
Kallikrein	RAYSEKVT	186	8	-0.0001	-0.0001	0.0003	0.0001	-0.0001	841
Kallikrein	RAYSEKVTEFM	186	11	0.0007	0.0560	0.0016	0.0018	0.0009	842
PSM	RIYNVIGT	354	8						843
PSM	RIYNVIGTL	354	9	0.0004					844
PSM	RLGIASGRA	527	9	0.0001					845
PAP	RLHPYKDFI	180	9	0.0006					846
PAP	RLHPYKDFIA	180	10	0.0048					847
PAP	RLHPYKDFIAT	180	11						848
PSM	RLLQERGV	440	8						849
PSM	RLLQERGVA	440	9	0.0001					850
PSM	RLLQERGVAYI	440	11						851
PSM	RLQDFDKSNPI	649	11						852

Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PAP	RLQGGVLV	257	8						853
PAP	RLQGGVLVNEI	257	11						854
PSA	RLSEPAEL	121	8	0.0004					855
PSA	RLSEPAELT	121	9	0.0003					856
PSA	RLSEPAELTDA	121	11	0.0007					857
Kallikrein	RLSEPAKI	125	8	-0.0001	0.0005	0.0007	-0.0001	-0.0001	858
Kallikrein	RLSEPAKIT	125	9	-0.0001	-0.0002	0.0009	-0.0001	-0.0002	859
Kallikrein	RLSEPAKITDV	125	11	0.0015	0.0043	0.0210	0.0002	0.0006	860
PSM	RMMNDQLM	662	8						861
PSM	RMMNDQLMFL	662	10	0.5100	1.6000	1.3000	0.0930	0.0005	862
PSM	RQIYVAAFT	730	9						863
PSM	RQIYVAAFTV	730	10						864
PSM	RTEDFFKL	181	8						865
PSM	RTILFASWDA	414	10						866
PAP	RTLMSAMT	111	8						867
PAP	RTLMSAMTNL	111	10	0.0150					868
PAP	RTLMSAMTNLA	111	11						869
PSM	RVDCTPLM	463	8						870
PSM	RVDCTPLMYSL	463	11						871
PSM	SAFSPQGM	162	8						872
PAP	SAHDTTVSGL	287	10	0.0002					873
PAP	SAMTNLAA	115	8						874
PAP	SAMTNLAAL	115	9	0.0043					875
PSM	SAVKNFTEI	634	9	0.0001					876
PSM	SAVKNFTEIA	634	10						877
Kallikrein	SIALSVGCT	7	9	-0.0001	0.0006	0.0087	0.0006	0.0004	878
Kallikrein	SIALSVGCTGA	7	11	0.0029	0.0066	0.0160	0.0100	0.0055	879
PSM	SIEGNYTL	455	8						880
PSM	SIEGNYTLRV	455	10	0.0001					881
Kallikrein	SIEPEEFL	159	8	0.0001					882
PSA	SIEPEEFL	155	8	0.0001					883
PSA	SIEPEEFLT	155	9	0.0001					884
PSM	SINEDGNEI	129	10	0.0001					885
PSM	SISMKHPQEM	613	10						886
PAP	SIWNPILL	130	8						887
PSA	SLFIPEDT	75	8	0.0003	0.0032	0.0028	-0.0001	-0.0001	888
PSA	SLFIPEDTGQV	75	11	0.0190					889
PSM	SLFSAVKNFT	631	10	0.0010					890
PAP	SLGFLFLL	15	8						891
Kallikrein	SLHLLSNDM	175	9	0.0003	0.0720	0.0180	-0.0001	0.0004	892
Kallikrein	SLHLLSNDMCA	175	11	0.0390	1.9000	0.6900	0.0005	0.0004	893
PSM	SLKVPYNV	322	8						894
Kallikrein	SLLKHQSL	104	8	0.0002	0.0007	0.0002	-0.0001	-0.0001	895
PSA	SLLKNRFL	100	8	0.0020					896
PAP	SLLSLYGI	242	8						897
Kallikrein	SLQCVSLHL	170	9	0.0100	0.0840	0.0240	0.0006	0.0031	898

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Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
Kallikrein	SLQCVSLHLL	170	10	0.0099	0.4000	0.0920	0.0059	0.0008	899
PAP	SLSLGFLFL	13	9	0.0200					900
PAP	SLSLGFLFLL	13	10	0.0170					901
PSM	SLVIINLTKEL	472	10	0.0002					902
PSM	SMKHPQEM	615	8						903
PSM	SMKHPQEMKT	615	10	0.0001					904
Kallikrein	SQPWQVAV	35	8						905
PSA	SQPWQVLV	31	8						906
PSA	SQPWQVLVA	31	9						907
Kallikrein	SQVWLGRHNL	71	10						908
PSM	SQWKEFGL	98	8						909
PSM	SQWKEFGLDSV	98	11						910
PSA	STCSGDSGGPL	203	11	0.0005	0.0150	0.0092	0.0002	0.0035	911
PAP	STDVDRTL	106	8						912
PAP	STDVDRTLM	106	9						913
PAP	STDVDRTLMSA	106	11						914
PSM	STEWAEENSRL	431	11						915
PSM	STNEVTRI	348	8						916
PSM	STNEVTRIYNV	348	11						917
PSM	STQKVKMHI	338	9	0.0001					918
PSM	SVELAHYDV	107	9	0.0001					919
PSM	SVELAHYDVL	107	10	0.0002					920
PSM	SVELAHYDVLL	107	11						921
Kallikrein	SVGCTGAV	11	8	0.0004	0.0006	0.0022	0.0003	-0.0001	922
Kallikrein	SVGCTGAVPL	11	10	0.0024	0.0760	0.0065	0.0026	0.0035	923
Kallikrein	SVGCTGAVPLI	11	11	0.0100	0.0010	0.0007	0.0007	0.0005	924
PAP	SVHNFTLPSWA	217	11						925
PSA	SVILLGRHSL	67	10	0.0001					926
PAP	SVLAKELKFV	29	10	0.0031					927
PAP	SVLAKELKFVT	29	11						928
PSM	SVSFDSLFSA	626	10						929
PSM	SVSFDSLFSAV	626	11						930
PSA	SVTWIGAA	7	8	0.0001					931
PSA	SVTWIGAAPL	7	10	0.0001					932
PSA	SVTWIGAAPLI	7	11	0.0001					933
PSM	SVYETYEL	554	8						934
PSM	SVYETYELV	554	9	0.0073					935
PSA	TAAHCIRNKSV	58	11	0.0005	0.0057	0.0085	0.0004	0.0105	936
PSM	TARRPRWL	14	8						937
PSM	TARRPRWLCA	14	10						938
PSM	TILFASWDA	415	9						939
PAP	TLGKLSGL	190	8						940
PAP	TLKSEEFQKRL	171	11						941
PAP	TLMSAMTNL	112	9	0.0650					942
PAP	TLMSAMTNLA	112	10	0.0065					943
PAP	TLMSAMTNLAA	112	11						944

Table VIII

Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PAP	TLPSWATEDT	222	10	0.0002					945
PAP	TLPSWATEDTM	222	11						946
PSM	TLRVDCTPL	461	9	0.0012					947
PSM	TLRVDCTPLM	461	10	0.0008					948
PSA	TLSVTWIGA	5	9	0.0016					949
PSA	TLSVTWIGAA	5	10	0.0007					950
PAP	TMTKLREL	231	8						951
PAP	TMTKLRELSEL	231	11						952
Kallikrein	TQEPALGT	143	8						953
PSA	TQEPALGT	139	8						954
Kallikrein	TQEPALGTT	143	9						955
PSA	TQEPALGTT	139	9						956
PAP	TQHEPYPL	335	8						957
PAP	TQHEPYPLM	335	9						958
PAP	TQHEPYPLML	335	10						959
PSM	TQIPHLAGT	78	9						960
PAP	TQIPSYKKL	275	9						961
PAP	TQIPSYKKLI	275	10						962
PAP	TQIPSYKKLIM	275	11						963
PSM	TQKVKMHI	339	8						964
PSM	TQKVKMHIIST	339	11						965
PAP	TQLGMEQHYEL	71	11						966
Kallikrein	TTCYASGWGSI	150	11	-0.0001	0.0009	0.0025	0.0005	0.1400	967
PSA	TTCYASGWGSI	146	11	-0.0001	0.0009	0.0025	0.0005	0.1400	968
PAP	TTNSHQGT	374	8						969
PAP	TTVSGLQM	291	8						970
PAP	TTVSGLQMA	291	9						971
PAP	TTVSGLQMAL	291	10	0.0020					972
PSM	TVAQVRGGM	575	9						973
PSM	TVAQVRGGMV	575	10	0.0005					974
PAP	TVPLSEDQL	145	9	0.0002					975
PAP	TVPLSEDQLL	145	10	0.0001					976
PSM	TVQAAAET	738	8						977
PSM	TVQAAAETL	738	9	0.0002					978
PAP	TVSGLQMA	292	8						979
PAP	TVSGLQMAL	292	9	0.0044					980
PAP	TVSGLQMALDV	292	11						981
PSM	VAAFTVQA	734	8						982
PSM	VAAFTVQAA	734	9						983
PSM	VAAFTVQAAA	734	10						984
PSM	VAQVRGGM	576	8						985
PSM	VAQVRGGMV	576	9	0.0002					986
PSA	VASRGRAV	38	8	-0.0001	-0.0001	-0.0001	-0.0001	-0.0001	987
PSM	VATARRPRWL	12	10	0.0001					988
Kallikrein	VAVYSHGWA	40	9	-0.0001	-0.0001	0.0002	0.0002	0.0004	989
PSM	VAYINADSSI	447	10	0.0001					990

Table VIII

Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PSM	VIARYGKV	201	8						991
PSM	VIGTLRGA	358	8						992
PSM	VIGTLRGAV	358	9	0.0002					993
PSM	VILGGHRDSWV	372	11						994
PSA	VILLGRHSL	68	9	0.0003					995
PSM	VILYSDPA	225	8						996
PAP	VIPQDWST	363	8						997
PAP	VIPQDWSTECM	363	11						998
PSA	VISNDVCA	174	8	0.0001					999
PSA	VISNDVCAQV	174	10	0.0008					1000
PSM	VLAGGFFL	27	8						1001
PSM	VLAGGFFLL	27	9	0.1300	19.0000	0.3000	0.1200	0.0028	1002
PAP	VLAKELKFV	30	9	0.0590					1003
PAP	VLAKELKFVT	30	10	0.0021					1004
PAP	VLAKELKFVTL	30	11						1005
Kallikrein	VLGLPTQEPA	138	10	0.0008	0.0150	0.0110	0.0004	-0.0001	1006
Kallikrein	VLGLPTQEPAL	138	11	-0.0001	0.0007	0.0003	0.0003	0.0006	1007
PSM	VLLSYPNKT	115	9	0.0002					1008
PSM	VLPFDCRDYA	592	10	0.0013					1009
PSM	VLPFDCRDYAV	592	11						1010
PSM	VLRKYADKI	603	9	0.0002					1011
PSM	VLRMMNDQL	660	9	0.0001					1012
PSM	VLRMMNDQLM	660	10	0.0003					1013
Kallikrein	VLSIALSV	5	8	0.0050	0.0790	0.0200	0.0024	0.0003	1014
Kallikrein	VLSIALSVGCT	5	11	0.0002	0.0011	0.0048	0.0004	0.0005	1015
PSA	VLTAAHCI	56	8	0.0001					1016
Kallikrein	VLTAAHCL	60	8	0.0002	0.0034	0.0001	0.0001	0.0002	1017
PSA	VLVASRGRA	36	9	0.0001					1018
PSA	VLVASRGRAV	36	10	0.0003					1019
Kallikrein	VLVHPQWV	53	8	0.0001					1020
PSA	VLVHPQWV	49	8	0.0001					1021
Kallikrein	VLVHPQWVL	53	9	0.0200					1022
PSA	VLVHPQWVL	49	9	0.0200					1023
Kallikrein	VLVHPQWVLT	53	10	0.0001					1024
PSA	VLVHPQWVLT	49	10	0.0001					1025
Kallikrein	VLVHPQWVLTA	53	11	0.0130					1026
PSA	VLVHPQWVLTA	49	11	0.0130					1027
PAP	VLVNEILNHM	262	10	0.0008					1028
PSA	VMDLPTQEPA	134	10	0.0001					1029
PSA	VMDLPTQEPAL	134	11	0.0021	0.0042	0.0014	0.0001	0.0003	1030
PSM	VQAAAETL	739	8						1031
PSM	VQAAAETLSEV	739	11						1032
PSM	VQRGNILNL	253	9						1033
Kallikrein	VTEFMLCA	192	8	-0.0001	0.0003	0.0005	0.0007	0.0007	1034
Kallikrein	VTEFMLCAGL	192	10	0.0008	0.0180	0.0068	0.0004	0.0030	1035
PSA	VTKFMLCA	188	8	0.0001	0.0002	0.0031	-0.0001	-0.0001	1036

Table VII

Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PSM	VTRIYNVI	352	8						1037
PSM	VTRIYNVIGT	352	10						1038
PSM	VTRIYNVIGTL	352	11						1039
PSA	VTWIGAAPL	8	9	0.0110					1040
PSA	VTWIGAAPLI	8	10	0.0019					1041
PSA	VTWIGAAPLIL	8	11	0.0013	0.0005	0.0009	0.0011	0.0002	1042
PSA	VVFLTLSV	1	8	0.0002					1043
PSA	VVFLTLSVT	1	9	0.0008					1044
PSA	VVFLTLSVTWI	1	11	0.0069					1045
PSM	VVIHEIVRSFGT	394	11						1046
Kallikrein	VVIIYRKWI	246	8	0.0001	0.0021	-0.0001	0.0001	-0.0001	1047
PSA	VVIIYRKWI	242	8	0.0001	0.0021	-0.0001	0.0001	-0.0001	1048
Kallikrein	VVIIYRKWIKDT	246	11	0.0001	0.0001	0.0002	-0.0001	0.0004	1049
PSA	VVIIYRKWIKDT	242	11	0.0001	0.0001	0.0002	-0.0001	0.0004	1050
Kallikrein	VVKVLGLPT	135	9	-0.0001	-0.0005	0.0007	0.0008	-0.0002	1051
PSM	VVLRKYADKI	602	10	0.0001					1052
PSM	WAEENSRL	434	8						1053
PSM	WAEENSRLL	434	9	0.0001					1054
Kallikrein	WAIICGGVL	47	8	-0.0001	0.0003	0.0005	0.0001	0.0070	1055
Kallikrein	WAIICGGVLV	47	9	-0.0001	0.0004	0.0067	0.0007	0.0310	1056
PAP	WATEDTMT	226	8						1057
PAP	WATEDTMTKL	226	10	0.0002					1058
PSA	WIGAAPLI	10	8	0.0005					1059
PSA	WIGAAPLIL	10	9	0.0005					1060
Kallikrein	WIKDTIAA	252	8	0.0002	0.0120	0.1700	0.0002	-0.0001	1061
PSA	WIKDTIVA	248	8	0.0001					1062
PSM	WLCAGALV	20	8						1063
PSM	WLCAGALVL	20	9	0.0180					1064
PSM	WLCAGALVLA	20	10	0.0120					1065
PAP	WLDRSVLA	25	8						1066
PAP	WLDRSVLAKEL	25	11						1067
PAP	WQPIPVHT	138	8						1068
PAP	WQPIPVHTV	138	9						1069
PAP	WQPIPVHTVPL	138	11						1070
Kallikrein	WQVAVYSHGWA	38	11						1071
PSA	WQVLVASRGRA	34	11						1072
PSA	WVLTAAHCI	55	9	0.0008					1073
Kallikrein	WVLTAAHCL	59	9	0.0003	0.0018	0.0001	0.0160	0.0007	1074
PSM	YADKIYSI	607	8						1075
PSM	YADKIYSISM	607	10						1076
PSM	YAGESFPGI	700	9	0.0013					1077
PSM	YAPSSHNKYA	692	10						1078
PSM	YARTEDFFKL	179	10	0.0002					1079
PAP	YASCHLTEL	310	9	0.0037					1080
Kallikrein	YASGWGSI	153	8	-0.0001	0.0009	0.0003	0.0003	0.0120	1081
PSA	YASGWGSI	149	8	-0.0001	0.0009	0.0003	0.0003	0.0120	1082

Table VII

Prostate A02 Supermotif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	A*0201	A*0202	A*0203	A*0206	A*6802	Seq. Id. No.
PSM	YAVVLRKYA	600	9						1083
PSM	YAYRRGIA	277	8						1084
PSM	YAYRRGIAEA	277	10						1085
PSM	YAYRRGIAEAV	277	11						1086
PSM	YINADSSI	449	8						1087
PAP	YIRKRYRKFL	84	10	0.0002					1088
PAP	YIRSTDVDRT	103	10						1089
PAP	YIRSTDVDRTL	103	11						1090
Kallikrein	YTKVVHYRKWI	243	11	0.0001	-0.0001	0.0004	-0.0001	0.0008	1091
FSA	YTKVVHYRKWI	239	11	0.0001	-0.0001	0.0004	-0.0001	0.0008	1092
PSM	YTLRVDCT	460	8						1093
PSM	YTLRVDCTPL	460	10	0.0015					1094
PSM	YTLRVDCTPLM	460	11						1095
PSM	YVAAFTVQA	733	9						1096
PSM	YVAAFTVQAA	733	10						1097
PSM	YVAAFTVQAAA	733	11						1098

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Protein	Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	Seq. Id. No.
PSA	AAHCIRNK	59	8						1099
PSA	AAPLILSR	13	8						1100
PAP	AAPLLLAR	3	8						1101
PSM	AAVVHEIVR	392	9						1102
PSM	ALFDIESK	711	8						1103
Kallikrein	ALPEKPAVYTK	235	11						1104
PSA	ALPERPSLYTK	231	11						1105
PSM	ASGRARYTK	531	9	0.0086	0.2700				1106
PAP	ATEDTMTK	227	8	0.0003	0.0039				1107
PAP	ATEDTMTKLR	227	10						1108
PSM	ATNITPKHNMK	49	11						1109
PAP	ATQIPSYK	274	8	0.0180	0.0700				1110
PAP	ATQIPSYKK	274	9	0.1000	1.2000				1111
PSM	AVATARRPR	11	9						1112
PSM	AVKNFTEIASK	635	11						1113
Kallikrein	AVPLIQSR	17	8						1114
PSM	AVVHEIVR	393	8						1115
PSM	AVVLRKYADK	601	10	0.0026	0.0210				1116
Kallikrein	AVYTKVVHYR	241	10						1117
Kallikrein	AVYTKVVHYRK	241	11						1118
Kallikrein	CAGLWTGGK	198	9						1119
PSA	CAGRWTGGK	194	9	0.0006	0.0015				1120
PSA	CAQVHPQK	180	8						1121
PSA	CAQVHPQKVTK	180	11						1122
Kallikrein	CARAYSEK	184	8						1123
PSM	CSGKIVIAR	196	9						1124
PAP	CSPSCPLER	347	9	0.0040	0.0006				1125
Kallikrein	CTGAVPLIQSR	14	11						1126
PSM	DALFDIESK	710	9	0.0006	0.0002				1127
PSM	DAQKLLEK	301	8						1128
PSM	DIESKVDPSK	714	10	0.0003	0.0002				1129
PAP	DLFGIWSK	201	8						1130
PSM	DLVYVNYAR	173	9						1131
Kallikrein	DMCARAYSEK	182	10						1132
PSM	DMKINCSGK	191	9						1133
PSA	DMSLLKNR	98	8	0.0003	0.0001				1134
PSA	DMSLLKNRFLR	98	11						1135
PSM	DSAVATAR	9	8						1136
PSM	DSAVATARR	9	9						1137
PSM	DSAVATARRPR	9	11						1138
PSM	DSLFSAVK	630	8						1139
Kallikrein	DSSHDLMLLR	116	10						1140
PSA	DSSHDLMLLR	112	10						1141
PSM	DSSIEGNYTLR	453	11						1142
PSM	DSSWRGSLK	316	9	0.0032	0.0003				1143
PAP	DTFPTDPIK	51	9	0.0001	0.0001				1144

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Protein	Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	Seq. Id. No.
PSA	DVCAQVHPQK	178	10	0.0007	0.0011				1145
PSM	DVLLSYPNK	114	9	0.0006	0.0010				1146
PSM	EATNITPK	48	8						1147
PSM	EIASKFSER	641	9	0.0006	0.0002				1148
PAP	EILNHMKR	266	8						1149
PSM	EIVRSFGTLK	397	10						1150
PSM	EIVRSFGTLKK	397	11						1151
PAP	ELESETLK	166	8						1152
PAP	ELGEYIRK	80	8						1153
PAP	ELGEYIRKR	80	9						1154
PAP	ELGEYIRKRYR	80	11						1155
PSM	ELKAENIK	64	8						1156
PSM	ELKAENIKK	64	9						1157
PAP	ELKFVTLVFR	34	10	0.0014	0.0037				1158
PSM	ESKVDPSK	716	8						1159
PAP	ESYKHEQVYIR	95	11						1160
PSM	ETDSAVATAR	7	10						1161
PSM	ETDSAVATARR	7	11						1162
PAP	ETLKSEEFQK	170	10	0.0004	0.0140				1163
PAP	ETLKSEEFQKR	170	11						1164
PSM	ETYELVEK	557	8						1165
PSM	FIDPLGLPDR	675	10						1166
PSM	FLDELKAENIK	61	11						1167
PSM	FLEGWFIK	37	8						1168
PAP	FLFLLFFWLDR	18	11						1169
PAP	FLLFFWLDR	20	9	0.0024	0.0004				1170
PSM	FSERLQDFDK	646	10	0.0003	0.0007				1171
PSM	FSGMPRISK	506	9						1172
PSM	FTEIASKFSER	639	11						1173
PSM	FTGNFSTQK	333	9						1174
PSM	FTGNFSTQKVK	333	11						1175
PAP	FVTLVFRHGDR	37	11						1176
PSA	GAAPLILSR	12	9	0.0150	0.0350				1177
PSM	GAAVVHEIVR	391	10						1178
Kallikrein	GAVPLIQSR	16	9						1179
PSM	GIASGRAR	529	8						1180
PSM	GIASGRARYTK	529	11						1181
PAP	GIHKQKEK	248	8						1182
PAP	GIHKQKEKSR	248	10						1183
PSM	GLPDRPFYR	680	9	0.0460	0.0280				1184
PSM	GSAPPDSSWR	311	10	0.0006	0.1400				1185
PSA	GSEPCALPER	226	10						1186
Kallikrein	GSIEPEEFLR	158	10						1187
PSM	GSTEWAEENSR	430	11						1188
PSM	GTEQNFQLAK	85	10						1189
PSM	GTLKKEGWR	403	9						1190

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Protein	Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	Seq. Id. No.
PSM	GTLKKEGWRPR	403	11						1191
PSM	GTLRGAVEPDR	360	11						1192
PSM	HHISTNEVTR	345	10						1193
Kallikrein	HLLSNDMCAR	177	10						1194
PAP	HLTELYFEK	314	9	0.2700	0.5300				1195
PSM	HLTVAQVR	573	8						1196
PSM	HSTNEVTR	347	8						1197
PSM	HVIYAPSSHNK	689	11						1198
PSM	IARYGKVFR	202	9						1199
PSM	IASGRARYTK	530	10						1200
PSM	IASKFSER	642	8						1201
PSM	ISMKHPQEMK	614	10	0.1900	0.1100				1202
PSM	ITPKHNMK	52	8						1203
Kallikrein	IVGGWECEK	25	9	0.0410	0.0190	0.0002	0.0006	0.0018	1204
PSA	IVGGWECEK	21	9	0.0410	0.0190	0.0002	0.0006	0.0018	1205
PSM	IVIARYGK	200	8						1206
PSM	IVIARYGKVFR	200	11						1207
PSM	IVLPFDCR	591	8						1208
PSM	IVRSFGTLK	398	9	0.1700	0.0087				1209
PSM	IVRSFGTLKK	398	10	0.0260	0.0006				1210
PSM	KAFLDELK	59	8						1211
PSM	KAWGEVKR	723	8						1212
PSM	KIVIARYGK	199	9	0.0740	1.0000				1213
PSM	KIYSISMK	610	8						1214
PAP	KSEEFQKR	173	8						1215
PSM	KSLYESWTK	491	9	0.4000	2.1000				1216
PSM	KSLYESWTKK	491	10	0.3200	0.0810				1217
PSM	KSNPIVLR	655	8						1218
PSM	KSPDEGFEGK	482	10	0.0044	0.0210				1219
PSA	KSVILLGR	66	8						1220
PSM	KVFRGNKVK	207	9	0.1600	0.1200				1221
PSM	KVKNAQLAGAK	213	11						1222
PSA	KVTKFMLCAGR	187	11						1223
Kallikrein	KVVHYRKWIK	245	10	0.0450	0.0450				1224
PSA	KVVHYRKWIK	241	10	0.0450	0.0450				1225
PSM	LAKQIQSQWK	92	10	0.0031	0.0007				1226
PAP	LLFFWLDR	21	8						1227
PSM	LLGFLFGWFIK	34	11						1228
Kallikrein	LLKHQSLR	105	8						1229
PSA	LLKNRFLR	101	8						1230
Kallikrein	LLRLSEPAK	123	9						1231
PAP	LLSLYGHIK	243	9	0.0760	0.2000				1232
PAP	LLSLYGHIKQK	243	11						1233
Kallikrein	LLSNDMCAR	178	9						1234
PAP	LLYLPFRNCPR	153	11						1235
Kallikrein	LMLLRLSEPAK	121	11						1236

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Protein	Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	Seq. Id. No.
PSM	LMYSLVHNLTK	469	11						1237
PAP	LSLLSLYGHIK	241	11						1238
PAP	LSLYGHIK	244	8						1239
PAP	LSLYGHIKQK	244	10	0.0520	0.0370				1240
Kallikrein	LSNDMCAR	179	8						1241
PSA	LTAAHCIR	57	8						1242
PSA	LTAAHCIRNK	57	10	0.1400	0.0830				1243
Kallikrein	LTAAHCLK	61	8						1244
Kallikrein	LTAAHCLKK	61	9						1245
PAP	LTELYFEK	315	8	0.0014	0.0100				1246
PSM	LVEKFYDPMFK	561	11						1247
PAP	LVFRHGDR	40	8	0.0003	0.0002				1248
PSM	LVHNLTKELK	473	10						1249
PAP	LVNEILNHMK	263	10	0.0560	0.1200				1250
PAP	LVNEILNHMKR	263	11						1251
PSM	LVYVNYAR	174	8						1252
Kallikrein	MLCAGLWTGGK	196	11						1253
PSA	MLCAGRWTGGK	192	11						1254
Kallikrein	MLLRLSEPAK	122	10						1255
PSM	MMNDQLMFLER	663	11						1256
Kallikrein	MSLLKHQSLR	103	10						1257
PSA	MSLLKNRFLR	99	10	0.0070	0.0110				1258
PSM	NAQLAGAK	216	8						1259
PSM	NITPKHNMK	51	9						1260
Kallikrein	NLFEPEDTGQR	79	11						1261
PSM	NLPGGGVQR	247	9						1262
PSM	NMKAFLDELK	57	10						1263
Kallikrein	NMSLLKHQSLR	102	11						1264
PSM	NSIVLPFDCR	589	10						1265
Kallikrein	NSQVWLGR	70	8						1266
PSM	NSRLLQER	438	8						1267
PSM	PADYFAPGVK	231	10						1268
PSA	PAELTDAVK	125	9	0.0002	0.0002	0.0004	0.0006	0.0001	1269
Kallikrein	PAKITDVVK	129	9						1270
PSM	PANEYAYR	273	8						1271
PSM	PANEYAYRR	273	9	0.0001	0.0002				1272
Kallikrein	PAVYTKVVHYR	240	11						1273
PAP	PIDTFPTDPIK	49	11						1274
PSM	PIGYYDAQK	296	9						1275
PSM	PLGLPDRPFYR	678	11						1276
PSA	PLYDMSLLK	95	9	0.2400	0.0370	0.0002	0.0006	0.0001	1277
PSA	PLYDMSLLKNR	95	11						1278
Kallikrein	PLYNMSLLK	99	9						1279
PSM	PSKAWGEVK	721	9						1280
PSM	PSKAWGEVKR	721	10	0.0003	0.0002				1281
PSA	PSLYTKVVHYR	236	11						1282

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Protein	Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	Seq. Id. No.
PSM	PSPEESGMPR	502	10						1283
PAP	PSWATEDTMTK	224	11						1284
PSM	QLAKQIQSQWK	91	11						1285
PAP	QLLYLPFR	152	8						1286
PSA	QVHPQKVTK	182	9	0.0060	0.0140	0.0028	0.0014	0.0051	1287
PSA	QVLVASRGR	35	9	0.0021	0.0018				1288
PAP	QVYIRSTDVDR	101	11						1289
PAP	RAAPLLLAR	2	9	0.1500	0.1200				1290
PAP	RATQIPSYK	273	9	0.0210	0.0600				1291
PAP	RATQIPSYKK	273	10	0.0053	0.0250				1292
Kallikrein	RIVGGWECEK	24	10	0.0460	0.0670				1293
PSA	RIVGGWECEK	20	10	0.0460	0.0670				1294
PSM	RIYNVIGTLR	354	10	0.3700	0.4300				1295
PSM	RLGIASGR	527	8						1296
PSM	RLGIASGRAR	527	10						1297
PSM	RSFGTLKK	400	8						1298
PAP	RSVLAKELK	28	9	0.0490	0.1100				1299
PSM	RTEDFFKLER	181	10						1300
PSM	SAPPDSSWR	312	9	0.0006	0.0012				1301
PSM	SAVATARR	10	8						1302
PSM	SAVATARRPR	10	10						1303
PSM	SIEGNYTLR	455	9						1304
Kallikrein	SIEPEEFLR	159	9						1305
Kallikrein	SIEPEEFLRPR	159	11						1306
PSA	SIEPEEFLTPK	155	11						1307
PSM	SISMKHPQEMK	613	11						1308
PSM	SIVLPFDCR	590	9	0.0006	0.0220				1309
Kallikrein	SLLKHQSLR	104	9						1310
PSA	SLLKNRFLR	100	9	0.0024	0.0470				1311
PAP	SLLSLYGHIK	242	10	0.4900	2.3000				1312
PSM	SLVHNLTK	472	8						1313
PSM	SLVHNLTKELK	472	11						1314
PSM	SLYESWTK	492	8						1315
PSM	SLYESWTKK	492	9	1.0000	2.0000				1316
PAP	SLYGIHKQK	245	9	1.1000	0.8000				1317
PAP	SLYGIHKQKEK	245	11						1318
PSA	SLYTKVVHYR	237	10	0.2800	0.2300				1319
PSA	SLYTKVVHYRK	237	11						1320
PSM	SMKHPQEMK	615	9	0.1100	0.0720				1321
Kallikrein	SSHDLMLLR	117	9	0.0039	1.2000				1322
PSA	SSHDLMLLR	113	9	0.0039	1.2000				1323
PSM	SSIEGNYTLR	454	10	0.0007	0.0910				1324
PSM	SSNEATNITPK	45	11						1325
PSM	SSWRGSLK	317	8						1326
PSM	STEWAEENSR	431	10	0.0005	0.0016				1327
PAP	SVLAKELK	29	8	0.0017	0.0061				1328

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Prostate A03 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	Seq. Id. No.
PSM	SVYETYELVEK	554	11						1329
PSA	TAAHCIRNK	58	9	0.0094	0.0140				1330
Kallikrein	TAAHCLKK	62	8						1331
PSM	TLKKEGWR	404	8						1332
PSM	TLKKEGWRPR	404	10	0.0007	0.0002				1333
PSM	TLKKEGWRPRR	404	11						1334
PAP	TLKSEEFQK	171	9	0.0006	0.0078				1335
PAP	TLKSEEFQKR	171	10	0.0007	0.0001				1336
PSM	TLRGAVEPDR	361	10	0.0003	0.0002				1337
PAP	TLVFRHGDR	39	9	0.0006	0.0002				1338
PSM	VATARRPR	12	8						1339
PSM	VIARYGKVFR	201	10						1340
PSM	VIYAPSSHNK	690	10	0.5400	0.7900				1341
PSM	VLLSYPNK	115	8						1342
PSM	VLRKYADK	603	8						1343
PSA	VLTAAHCIR	56	9	0.0002	0.0005				1344
PSA	VLTAAHCIRNK	56	11						1345
Kallikrein	VLTAAHCLK	60	9						1346
Kallikrein	VLTAAHCLKK	60	10						1347
PSA	VLVASRGR	36	8						1348
PAP	VLVNEILNHMK	262	11						1349
PSM	VSFDSLFSAVK	627	11						1350
PSA	VTKFMLCAGR	188	10	0.0003	0.0120				1351
PAP	VTLVFRHGDR	38	10						1352
Kallikrein	VVHYRKWIK	246	9	0.0072	0.0930	0.5500	0.0490	0.0028	1353
PSA	VVHYRKWIK	242	9	0.0072	0.0930	0.5500	0.0490	0.0028	1354
PSM	VVLRKYADK	602	9	0.0390	0.0660				1355
PAP	WATEDTMTK	226	9	0.0006	0.0002				1356
PAP	WATEDTMTKLR	226	11						1357
PSA	WIGAAPLILSR	10	11						1358
PAP	WLDRSVLAK	25	9	0.0035	0.0150				1359
PSA	WVLTAAHCIR	55	10	0.0004	0.0001				1360
Kallikrein	WVLTAAHCLK	59	10						1361
Kallikrein	WVLTAAHCLKK	59	11						1362
PSM	YADKIYSISMK	607	11						1363
PSM	YAPSSHNK	692	8						1364
PSM	YARTEDFFK	179	9						1365
PSM	YAVVLRKYADK	600	11						1366
PAP	YIRKRYRK	84	8						1367
PAP	YIRSTDVDR	103	9						1368
PAP	YLPFRNCPR	155	9						1369
PSM	YSLVHNLTK	471	9	0.0600	0.5400				1370
PSM	YTKNWETNK	537	9						1371
Kallikrein	YTKVVHYR	243	8						1372
PSA	YTKVVHYR	239	8						1373
Kallikrein	YTKVVHYRK	243	9	0.0006	0.0580	1.2000	2.8000	1.3000	1374

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Prostate A03 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	A*1101	A*3101	A*3301	A*6801	Seq. Id. No.
PSA	YTKVVHYRK	239	9	0.0006	0.0580	1.2000	2.8000	1.3000	1375
PSM	YVILGGHR	371	8						1376

Table X

Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PSM	AFIDPLGL	674	8		1377
PSM	AFLDELKAENI	60	11		1378
PSM	AFTVQAAAETL	736	11		1379
PAP	ALDVYNGL	299	8		1380
PAP	ALDVYNGLL	299	9		1381
PAP	ALFPPEGVSI	122	10		1382
PAP	ALFPPEGVSIW	122	11		1383
Kallikrein	ALGTTCYASGW	147	11		1384
PSA	ALGTTCYASGW	143	11		1385
Kallikrein	ALPEKPAVY	235	9		1386
PSA	ALPERPSL	231	8		1387
PSA	ALPERPSLY	231	9		1388
PSM	ALVLAGGF	25	8		1389
PSM	ALVLAGGFF	25	9		1390
PSM	ALVLAGGFFL	25	10		1391
PSM	ALVLAGGFFLL	25	11		1392
PAP	AMTNLAAL	116	8		1393
PAP	AMTNLAALF	116	9	0.0150	1394
PSM	ATARRPRW	13	8		1395
PSM	ATARRPRWL	13	9		1396
PAP	ATEDTMTKL	227	9		1397
PAP	ATLGKLSGL	189	9		1398
PSM	ATNITPKHNM	49	10		1399
PAP	ATQIPSYKKL	274	10		1400
PAP	ATQIPSYKKLI	274	11		1401
PSM	AVATARRPRW	11	10		1402
PSM	AVATARRPRWL	11	11		1403
PSM	AVEPDRYVI	365	9		1404
PSM	AVEPDRYVIL	365	10		1405
PSM	AVKNFTEI	635	8		1406
Kallikrein	AVPLIQSRI	17	9		1407
PSM	AVVHEIVRSF	393	10		1408
PSM	AVVLRKYADKI	601	11		1409
Kallikrein	AVYTKVVHY	241	9		1410
PSM	AWGEVKRQI	724	9		1411
PSM	AWGEVKRQIY	724	10		1412
PSM	AYINADSSI	448	9	0.0190	1413
Kallikrein	AYSEKVTEF	187	9		1414
Kallikrein	AYSEKVTEFM	187	10		1415
Kallikrein	AYSEKVTEFML	187	11		1416
PSA	CIRNKSVI	62	8		1417
PSA	CIRNKSVIL	62	9		1418
PSA	CIRNKSVILL	62	10		1419
Kallikrein	CLKKNSQVW	66	9		1420
Kallikrein	CLKKNSQVWL	66	10		1421
Kallikrein	CTGAVPLI	14	8		1422

Table X
Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PSM	CTPLMYSL	466	8		1423
Kallikrein	CVSLHLLSNDM	173	11		1424
Kallikrein	CYASGWGSI	152	9	0.1700	1425
PSA	CYASGWGSI	148	9	0.1700	1426
PSM	DFDKSNPI	652	8		1427
PSM	DFDKSNPIVL	652	10		1428
PSM	DFEVFFQRL	520	9		1429
PSM	DFEVFFQRLGI	520	11		1430
PSM	DFFKLERDM	184	9		1431
PSM	DFFKLERDMKI	184	11		1432
PAP	DFIATLGKL	186	9	0.0002	1433
PSM	DIVPPFSAF	156	9		1434
PAP	DLFGIWSKVY	201	10		1435
PSA	DLPTQEPAL	136	9		1436
Kallikrein	DLVLSIAL	3	8		1437
PSM	DMKINCSGKI	191	10		1438
PSA	DMSLLKNRF	98	9	0.0001	1439
PSA	DMSLLKNRFL	98	10		1440
Kallikrein	DTCGGDSGGPL	207	11		1441
PAP	DTFPTDPI	51	8		1442
PAP	DTMTKLREL	230	9		1443
PAP	DTTVSGLQM	290	9		1444
PAP	DTTVSGLQMAL	290	11		1445
PAP	DVDRTLMSAM	108	10		1446
Kallikrein	DVVKVLGL	134	8		1447
PAP	DVYNGLLPPY	301	10		1448
PSM	DYAVVLRKY	599	9		1449
PSM	DYFAPGVKSY	233	10		1450
PSM	EFGLDSVEL	102	9		1451
PSM	EFGLLGSTEW	425	10		1452
Kallikrein	EFLRPRSL	164	8		1453
PSA	EFLTPKKL	160	8		1454
Kallikrein	EFMLCAGL	194	8		1455
Kallikrein	EFMLCAGLW	194	9		1456
PAP	EFQKRLHPY	176	9		1457
PSM	EFSGMPRI	505	8		1458
PSM	EFSGMPRISKL	505	11		1459
PSM	EIASKFSERL	641	10		1460
PSM	EIFNTSLF	137	8		1461
PSM	EIVRSFGTL	397	9		1462
PSM	ELAHYDVL	109	8		1463
PSM	ELAHYDVLL	109	9		1464
PSM	ELAHYDVLLSY	109	11		1465
PSM	ELANSIVL	586	8		1466
PSM	ELANSIVLPF	586	10		1467
PAP	ELGEYIRKRY	80	10		1468

Table X
Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PSM	ELKAENIKKF	64	10		1469
PSM	ELKAENIKKFL	64	11		1470
PAP	ELKFVTLVF	34	9		1471
PSM	ELKSPDEGF	480	9		1472
PAP	ELSELSLL	237	8		1473
PAP	ELSELSLLSL	237	10		1474
PAP	ELSELSLLSLY	237	11		1475
PAP	ELSLLSLY	240	8		1476
PAP	ELSLLSLYGI	240	10		1477
PSA	ELTDAVKVM	127	9		1478
PSA	ELTDAVKVMDL	127	11		1479
PSM	ELVEKFYDPM	560	10		1480
PSM	ELVEKFYDPMF	560	11		1481
PAP	ELVGPVIPQDW	358	11		1482
PAP	ELYFEKGEY	317	9		1483
PAP	ELYFEKGEYF	317	10		1484
PSM	EMKTYSVSF	621	9	0.0010	1485
PAP	ETLKSEEF	170	8		1486
PSM	ETNKFSGY	542	8		1487
PSM	ETNKFSGYPL	542	10		1488
PSM	ETNKFSGYPLY	542	11		1489
PAP	ETQHEPYPL	334	9		1490
PAP	ETQHEPYPLM	334	10		1491
PAP	ETQHEPYPLML	334	11		1492
PSM	ETYELVEKF	557	9		1493
PSM	ETYELVEKFY	557	10		1494
PSM	EVFFQRLGI	522	9		1495
PSM	EVKRQIYVAAF	727	11		1496
PSM	EVTRIYNVI	351	9		1497
PSM	EWAEENSRL	433	9		1498
PSM	EWAEENSRLL	433	10		1499
PSM	EYAYRRGI	276	8		1500
PAP	EYFVEMYY	324	8		1501
PAP	EYIRKRYRKF	83	10	0.0067	1502
PAP	EYIRKRYRKFL	83	11		1503
PSM	FFKLERDM	185	8		1504
PSM	FFKLERDMKI	185	10		1505
PSM	FFLLGFLF	32	8		1506
PSM	FFLLGFLFGW	32	10	0.0026	1507
PSM	FFLLGFLFGWF	32	11		1508
PAP	FFWLDRSVL	23	9	0.0017	1509
PAP	FIATLGKL	187	8		1510
PAP	FIATLGKLSGL	187	11		1511
PSM	FIKSSNEATNI	42	11		1512
PSM	FLDELKAENI	61	10		1513
PSM	FLERAFIDPL	670	10		1514

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Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PAP	FLFLLFFW	18	8		1515
PAP	FLFLLFFWL	18	9		1516
PSM	FLLGFLFGW	33	9		1517
PSM	FLLGFLFGWF	33	10		1518
PSM	FLLGFLFGWFI	33	11		1519
PSA	FLTLSVTW	3	8		1520
PSA	FLTLSVTWI	3	9		1521
PSM	FLYNFTQI	73	8		1522
PSM	FLYNFTQIPHL	73	11		1523
Kallikrein	FMLCAGLW	195	8		1524
PSA	FMLCAGRW	191	8		1525
PSM	FTEIASKF	639	8		1526
PSM	FTVQAAAETL	737	10		1527
PAP	FWLDRSVL	24	8		1528
PSM	FYDPMFKY	565	8		1529
PSM	FYDPMFKYHL	565	10	1.1000	1530
PSM	GFEGKSLY	487	8		1531
PSM	GFEGKSLYESW	487	11		1532
PSM	GFFLLGFL	31	8		1533
PSM	GFFLLGFLF	31	9	0.0190	1534
PSM	GFFLLGFLFGW	31	11		1535
PAP	GFGQLTQL	66	8		1536
PAP	GFGQLTQLGM	66	10		1537
PSM	GFLFGWFI	36	8		1538
PAP	GFLFLLFF	17	8		1539
PAP	GFLFLLFFW	17	9	0.0016	1540
PAP	GFLFLLFFWL	17	10	0.0007	1541
PSM	GIAEAVGL	282	8		1542
PSM	GIAEAVGLPSI	282	11		1543
PSM	GIASGRARY	529	9		1544
PAP	GIHKQKEKSRL	248	11		1545
PAP	GIWSKVYDPL	204	10		1546
PAP	GIWSKVYDPLY	204	11		1547
PSM	GIYDALFDI	707	9		1548
PSM	GLDSVELAHY	104	10		1549
PAP	GLHGQDLF	196	8		1550
PAP	GLHGQDLFGI	196	10		1551
PAP	GLHGQDLFGIW	196	11		1552
PSM	GLLGSTEW	427	8		1553
PAP	GLLPPYASCHL	305	11		1554
PSM	GLPDRPFY	680	8		1555
PSM	GLPSIPVHPI	288	10		1556
Kallikrein	GLPTQEPAL	140	9		1557
PAP	GLQMALDVY	295	9		1558
PAP	GMEQHYEL	74	8		1559
PAP	GMEQHYELGEY	74	11		1560

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Prostate A24 Supermotif Peptides With Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PSM	GMPEGDLVY	168	9		1561
PSM	GMPRISKL	508	8		1562
PSM	GMVFELANSI	582	10	0.0002	1563
PSM	GTEQNFQL	85	8		1564
PSM	GTLKKEGW	403	8		1565
PSM	GTTCYASGW	149	9		1566
Kallikrein	GTTCYASGW	145	9		1567
PSA	GVAYINADSSI	446	11		1568
PSM	GVILYSDPADY	224	11		1569
PSM	GVKSYPDGW	238	9		1570
PSM	GVKSYPDGWNL	238	11		1571
PSM	GVLQGITSW	221	9		1572
Kallikrein	GVLQGITSW	217	9		1573
PSA	GVLVHPQW	52	8		1574
Kallikrein	GVLVHPQW	48	8		1575
PSA	GVLVHPQWVL	52	10		1576
Kallikrein	GVLVHPQWVL	48	10		1577
PSA	GVLVNEIL	261	8		1578
PAP	GVLVNEILNHM	261	11		1579
PAP	GVQRGNIL	252	8		1580
PSM	GVQRGNILNL	252	10		1581
PSM	GVSIWNPI	128	8		1582
PAP	GVSIWNPIL	128	9		1583
PAP	GVSIWNPILL	128	10		1584
PAP	GVSIWNPILLW	128	11		1585
PAP	GWAHCGGVL	46	9		1586
Kallikrein	GWECEKHSQPW	28	11		1587
Kallikrein	GWECEKHSQPW	24	11		1588
PSA	GWGSIEPEEF	156	10	0.0001	1589
Kallikrein	GWGSIEPEEF	152	10	0.0001	1590
PSA	GWGSIEPEEFL	156	11		1591
Kallikrein	GWGSIEPEEFL	152	11		1592
PSA	GWRPRRTI	409	8		1593
PSM	GWRPRRTIL	409	9		1594
PSM	GWRPRRTILF	409	10	0.0540	1595
PSM	GYENVSDI	150	8		1596
PSM	GYPANEYAY	271	9		1597
PSM	GYPLYHSVY	548	9		1598
PSM	GYYDAQKL	298	8		1599
PSM	GYYDAQKLL	298	9		1600
PSM	HHHSTNEVTRI	345	11		1601
PSM	HLAGTEQNF	82	9		1602
PSM	HLAGTEQNFQL	82	11		1603
PSM	HLTVAQVRGGM	573	11		1604
PAP	HMKRATQI	270	8		1605
PAP	HMKRATQIPSY	270	11		1606

Table X

Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PAP	HTVPLSEDQL	144	10		1607
PAP	HTVPLSEDQLL	144	11		1608
PSM	HYDVLLSY	112	8		1609
PAP	HYELGEYI	78	8		1610
Kallikrein	HYRKWIKDTI	248	10	0.0550	1611
PSA	HYRKWIKDTI	244	10	0.0550	1612
PSM	HNEDGNEI	130	9		1613
PSM	HNEDGNEIF	130	10		1614
PSM	ILFASWDAEEF	416	11		1615
PSM	ILGGHRDSW	373	9		1616
PSM	ILGGHRDSWVF	373	11		1617
PSA	ILLGRHSL	69	8		1618
PSA	ILLGRHSLF	69	9		1619
PAP	ILNHMKRATQI	267	11		1620
PSM	ILNLNGAGDPL	258	11		1621
PSA	ILSRIVGGW	17	9		1622
PSM	ILYSDPADY	226	9		1623
PSM	ILYSDPADYF	226	10		1624
Kallikrein	ITDVVKVL	132	8		1625
Kallikrein	ITDVVKVLGL	132	10		1626
PSM	ITPKHNMKAF	52	10		1627
PSM	ITPKHNMKAFL	52	11		1628
Kallikrein	ITSWGPEPCAL	226	11		1629
PSA	ITSWGSEPCAL	222	11		1630
PSM	IVIARYGKVF	200	10		1631
PSM	IVLPFDCRDY	591	10		1632
PSM	IVLRMMNDQL	659	10		1633
PSM	IVLRMMNDQLM	659	11		1634
PSM	IVPPFSAF	157	8		1635
PSM	IVRSFGTL	398	8		1636
PAP	IWNPILLW	131	8		1637
PAP	IWNPILLWQPI	131	11		1638
PAP	IWSKVYDPL	205	9	0.0024	1639
PAP	IWSKVYDPLY	205	10		1640
PSM	IYAPSSHNKY	691	10		1641
PSM	IYDALFDI	708	8		1642
PSM	IYNVIGTL	355	8		1643
PSM	KFLYNFTQI	72	9		1644
PSA	KFMLCAGRW	190	9	0.0310	1645
PSM	KFSERLQDF	645	9		1646
PSM	KFSGYPLY	545	8		1647
PSM	KFYDPMFKY	564	9		1648
PSM	KFYDPMFKYHL	564	11		1649
PSM	KINCSGKI	193	8		1650
PSM	KINCSGKIVI	193	10		1651
Kallikrein	KITDVVKVL	131	9		1652

Table X

Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
Kallikrein	KITDVVKVLGL	131	11		1653
PSM	KIVIARYGKVF	199	11		1654
PSM	KLERDMKI	187	8		1655
PSM	KLGSGNDF	514	8		1656
PSM	KLGSGNDFEVF	514	11		1657
PSA	KLQCVDLHVI	166	10		1658
PAP	KLRELSEL	234	8		1659
PAP	KLRELSELSL	234	10		1660
PAP	KLRELSELSLL	234	11		1661
PAP	KLSGLIIGQDL	193	10		1662
PAP	KLSGLIIGQDLF	193	11		1663
PSM	KTHPNYISI	122	9		1664
PSM	KTHPNYISII	122	10		1665
PSM	KTYSVSFDSL	623	10		1666
PSM	KTYSVSFDSLF	623	11		1667
PSM	KVDPSKAW	718	8		1668
PSM	KVPYNVGPGF	324	10		1669
Kallikrein	KVTEFMLCAGL	191	11		1670
Kallikrein	KVVHYRKW	245	8		1671
PSA	KVVHYRKW	241	8		1672
Kallikrein	KVVHYRKWI	245	9		1673
PSA	KVVHYRKWI	241	9		1674
PSM	KYADKIYSI	606	9	12.0000	1675
PSM	KYADKIYSISM	606	11		1676
PSM	KYAGESFPGI	699	10		1677
PSM	KYAGESFPGIY	699	11		1678
PSM	LFASWDAEEF	417	10		1679
PSM	LFEPPPPGY	143	9		1680
PAP	LFFWLDRSVL	22	10	0.0045	1681
PAP	LFGIWSKVY	202	9		1682
PSA	LFHPEDTGQVF	76	11		1683
PAP	LFLLFFWL	19	8		1684
PAP	LFPPEGVSI	123	9	0.0033	1685
PAP	LFPPEGVSIW	123	10	0.0140	1686
PSM	LFSAVKNF	632	8		1687
PSM	LFSAVKNFTEI	632	11		1688
PSA	LILSRIVGGW	16	10		1689
Kallikrein	LIQSRIVGGW	20	10		1690
PAP	LLARAASL	7	8		1691
PAP	LLARAASLSL	7	10		1692
PAP	LLFFWLDRSVL	21	11		1693
PSM	LLGFLFGW	34	8		1694
PSM	LLGFLFGWF	34	9		1695
PSM	LLGFLFGWFI	34	10		1696
PSA	LLGRHSLF	70	8		1697
PAP	LLLARAASL	6	9		1698

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Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PAP	LLLARAASLSL	6	11		1699
PAP	LLPPYASCHL	306	10		1700
PSM	LLQERGVAY	441	9		1701
PSM	LLQERGVAYI	441	10		1702
PSA	LLRLSEPAEL	119	10		1703
Kallikrein	LLRLSEPAKI	123	10		1704
Kallikrein	LLSNDMCARAY	178	11		1705
PSM	LMFLERAF	668	8		1706
PSM	LMFLERAFI	668	9	0.0075	1707
PAP	LMSAMTNL	113	8		1708
PAP	LMSAMTNLAAL	113	11		1709
PSM	LMYSLVHNL	469	9		1710
PSA	LTDAVKVM	128	8		1711
PSA	LTDAVKVMDL	128	10		1712
PAP	LTELYFEKGEY	315	11		1713
PSA	LTLSVTWI	4	8		1714
PSM	LTPGYPANEY	268	10		1715
PSA	LTPKKLQCVDL	162	11		1716
PAP	LTQLGMEQHY	70	10	0.0022	1717
PSM	LTVAQVRGGM	574	10		1718
Kallikrein	LVCNGVLQGI	217	10		1719
PSA	LVCNGVLQGI	213	10		1720
PSM	LVEKFYDPM	561	9		1721
PSM	LVEKFYDPMF	561	10		1722
PAP	LVFRHGDRSPI	40	11		1723
PAP	LVGPVIPQDW	359	10		1724
PSM	LVHNLTKEL	473	9		1725
Kallikrein	LVHPQWVL	54	8		1726
PSA	LVHPQWVL	50	8		1727
PSM	LVLAGGFF	26	8		1728
PSM	LVLAGGFFL	26	9		1729
PSM	LVLAGGFFLL	26	10		1730
PAP	LVNEILNHM	263	9		1731
PAP	LYCESVHNF	213	9	0.4400	1732
PAP	LYCESVHNFTL	213	11		1733
PSA	LYDMSLLKNRF	96	11	0.1200	1734
PAP	LYFEKGEY	318	8		1735
PAP	LYFEKGEYF	318	9	2.5000	1736
PSM	LYHSVYETY	551	9		1737
PSM	LYHSVYETYEL	551	11		1738
PAP	LYLPFRNCPRF	154	11		1739
PSM	LYNFTQIPHL	74	10	0.2300	1740
PSM	LYSDPADY	227	8		1741
PSM	LYSDPADYF	227	9	0.4400	1742
PSA	LYTKVVHY	238	8		1743
PSA	LYTKVVHYRKW	238	11		1744

Table X

Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PSM	MFLERAFI	669	8		1745
PSM	MFLERAFIDPL	669	11		1746
PSA	MLLRLSEPAEL	118	11		1747
Kallikrein	MLLRLSEPAKI	122	11		1748
PAP	MLPGCSPSCPL	343	11		1749
PSM	MMNDQLMF	663	8		1750
PSM	MMNDQLMFL	663	9		1751
PAP	MTKLRELSEL	232	10		1752
PAP	MTNLAALF	117	8		1753
PSM	MVFELANSI	583	9		1754
PSM	MVFELANSIVL	583	11		1755
Kallikrein	MWDLVLSI	1	8		1756
Kallikrein	MWDLVLSIAL	1	10		1757
PSM	MYSLVHNL	470	8		1758
PSM	NFQLAKQI	89	8		1759
PSM	NFSTQKVKM	336	9		1760
PSM	NFSTQKVKMIH	336	11		1761
PSM	NFTEIASKF	638	9	0.0001	1762
PSM	NFTQIPHL	76	8		1763
PSM	NIKKFLYNF	69	9		1764
PSM	NITPKHNM	51	8		1765
PSM	NITPKHNMKAF	51	11		1766
PSM	NLNGAGDPL	260	9		1767
PSM	NMKAFLDEL	57	9		1768
Kallikrein	NMSLLKHQSL	102	10		1769
PSM	NVGPGFTGNF	328	10		1770
PSM	NVSDIVPPF	153	9		1771
PSM	NWETNKFSGY	540	10		1772
PSM	NYARTEDF	178	8		1773
PSM	NYARTEDFF	178	9	0.7700	1774
PSM	NYARTEDFFKL	178	11		1775
PSM	NYTLRVDCTPL	459	11		1776
PSM	PFDCRDYAVVL	594	11		1777
PAP	PFRNCPRF	157	8		1778
PAP	PFRNCPRFQEL	157	11		1779
PSM	PFSAFSPQGM	160	10		1780
PSM	PFYRHVIY	685	8		1781
PAP	PIDTFPTDPI	49	10		1782
PSM	PIGYYDAQKL	296	10		1783
PSM	PIGYYDAQKLL	296	11		1784
PAP	PIKESSWPQGF	57	11		1785
PAP	PILLWQPI	134	8		1786
PAP	PIPVHTVPL	140	9		1787
PSM	PIVLRMMNDQL	658	11		1788
PAP	PLEREAEL	352	8		1789
PSM	PLGLPDRPF	678	9		1790

Table X

Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Aci	A*2401	Seq. Id. No.
PSM	PLGLPDRPFY	678	10		1791
PSA	PLILSRIVGGW	15	11		1792
Kallikrein	PLIQSRIVGGW	19	11		1793
PAP	PLLLARAASL	5	10		1794
PSM	PLMYSLVHNL	468	10		1795
PAP	PLSEDQLL	147	8		1796
PAP	PLSEDQLLY	147	9		1797
PAP	PLSEDQLLYL	147	10		1798
PSM	PLTPGYPANEY	267	11		1799
Kallikrein	PLVCNGVL	216	8		1800
PSA	PLVCNGVL	212	8		1801
Kallikrein	PLVCNGVLQGI	216	11		1802
PSA	PLVCNGVLQGI	212	11		1803
PAP	PLYCESVHNF	212	10		1804
PSA	PLYDMSLL	95	8		1805
PSM	PLYHSVYETY	550	10		1806
Kallikrein	PLYNMSLL	99	8		1807
PAP	PTDPIKESSW	54	10		1808
PSM	PVHPIGYY	293	8		1809
Kallikrein	PVSHSFPHPL	91	10		1810
Kallikrein	PVSHSFPHPLY	91	11		1811
Kallikrein	PWQVAVYSHGW	37	11		1812
PAP	PYASCHLTEL	309	10	0.0240	1813
PAP	PYASCHLTELY	309	11		1814
PAP	PYKDFIATL	183	9	0.1100	1815
PSM	PYNVGPGF	326	8		1816
PAP	QIPSYKKL	276	8		1817
PAP	QIPSYKKLI	276	9		1818
PAP	QIPSYKKLIM	276	10		1819
PAP	QIPSYKKLIMY	276	11		1820
PSM	QIQSQWKEF	95	9		1821
PSM	QIQSQWKEFGL	95	11		1822
PSM	QLAGAKGVI	218	9		1823
PSM	QLAGAKGVIL	218	10		1824
PSM	QLAGAKGVILY	218	11		1825
PSM	QLAKQIQSQW	91	10		1826
PAP	QLGMEQHY	72	8		1827
PAP	QLGMEQHYEL	72	10		1828
PSM	QLMFLERAF	667	9		1829
PSM	QLMFLERAFI	667	10		1830
PAP	QLTQLGMEQHY	69	11		1831
PAP	QMALDVYNGL	297	10	0.0001	1832
PAP	QMALDVYNGLL	297	11		1833
Kallikrein	QVAVYSHGW	39	9		1834
PSA	QVFQVSHSF	84	9		1835
PSA	QVHPQKVTKF	182	10		1836

Table X

Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PSA	QVHPQKVTKFM	182	11		1837
PSM	QVRGGMVF	578	8		1838
PSM	QVRGGMVFEL	578	10		1839
PSA	QVSHSFPHPL	87	10		1840
PSA	QVSHSFPHPLY	87	11		1841
Kallikrein	QVWLGRHNL	72	9		1842
Kallikrein	QVWLGRHNLF	72	10		1843
PSA	QWVLTAAHCI	54	10	0.0007	1844
Kallikrein	QWVLTAAHCL	58	10		1845
PAP	RFAELVGPVI	355	10	0.0037	1846
PAP	RFQELESETL	163	10	0.0001	1847
PSM	RISKLGSGNDF	511	11		1848
PSM	RIYNVIGTL	354	9		1849
PSM	RLGIASGRARY	527	11		1850
PAP	RLHPYKDF	180	8		1851
PAP	RLHPYKDFI	180	9		1852
PSM	RLLQERGVAY	440	10		1853
PSM	RLLQERGVAYI	440	11		1854
PSM	RLQDFDKSNPI	649	11		1855
PAP	RLQGGVLVNEI	257	11		1856
PSA	RLSEPAEL	121	8		1857
Kallikrein	RLSEPAKI	125	8		1858
PSM	RMMNDQLM	662	8		1859
PSM	RMMNDQLMF	662	9		1860
PSM	RMMNDQLMFL	662	10		1861
PSM	RTEDFFKL	181	8		1862
PSM	RTILFASW	414	8		1863
PAP	RTLMSAMTNL	111	10		1864
PSM	RVDCTPLM	463	8		1865
PSM	RVDCTPLMY	463	9		1866
PSM	RVDCTPLMYSL	463	11		1867
Kallikrein	RVPVSHSF	89	8		1868
PSM	RWLCAGAL	19	8		1869
PSM	RWLCAGALVL	19	10		1870
PAP	RYRKFLNESY	88	10	0.0057	1871
PSM	RYTKNWETNKF	536	11		1872
PSM	SFGTLKKEGW	401	10		1873
PSM	SFPGIYDAL	704	9		1874
PSM	SFPGIYDALF	704	10		1875
PSA	SFPHPLYDM	91	9	0.0007	1876
PSA	SFPHPLYDMSL	91	11		1877
Kallikrein	SFPHPLYNM	95	9		1878
Kallikrein	SFPHPLYNMSL	95	11		1879
PSM	SIEGNYTL	455	8		1880
Kallikrein	SIEPEEFL	159	8		1881
PSA	SIEPEEFL	155	8		1882

Table X

Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PSM	SIINEDGNEI	129	10		1883
PSM	SIINEDGNEIF	129	11		1884
PSM	SIPVHIPIGY	291	9		1885
PSM	SIPVHIPIGYY	291	10		1886
PSM	SISMKHPQEM	613	10		1887
PSM	SIVLPFDCRDY	590	11		1888
PAP	SIWNPILL	130	8		1889
PAP	SIWNPILLW	130	9		1890
PSM	SLFEPPPPGY	142	10		1891
PSM	SLFSAVKNF	631	9		1892
PAP	SLGFLFLL	15	8		1893
PAP	SLGFLFLLF	15	9		1894
PAP	SLGFLFLLFF	15	10		1895
PAP	SLGFLFLLFFW	15	11		1896
Kallikrein	SLIILLSNDM	175	9		1897
Kallikrein	SLLKHQSL	104	8		1898
PSA	SLLKNRFL	100	8		1899
PAP	SLLSLYGI	242	8		1900
Kallikrein	SLQCVSLHL	170	9		1901
Kallikrein	SLQCVSLHLL	170	10		1902
PAP	SLSLGFLF	13	8		1903
PAP	SLSLGFLFL	13	9		1904
PAP	SLSLGFLFLL	13	10		1905
PAP	SLSLGFLFLLF	13	11		1906
PSM	SLVHNLTKEL	472	10		1907
PSA	SLYTKVVHY	237	9		1908
PSM	SMKHPQEM	615	8		1909
PSM	SMKHPQEMKTY	615	11		1910
PSA	STCSGDSGGPL	203	11		1911
PAP	STDVDRTL	106	8		1912
PAP	STDVDRTLM	106	9		1913
PSM	STEWAEENSRL	431	11		1914
PSM	STNEVTRI	348	8		1915
PSM	STNEVTRIY	348	9		1916
PSM	STQKVKMHI	338	9		1917
PSM	SVELAHYDVL	107	10		1918
PSM	SVELAHYDVLL	107	11		1919
Kallikrein	SVGCTGAVPL	11	10		1920
Kallikrein	SVGCTGAVPLI	11	11		1921
PAP	SVHNFTLPSW	217	10		1922
PSA	SVILLGRHSL	67	10		1923
PSA	SVILLGRHSLF	67	11		1924
PAP	SVLAKELKF	29	9		1925
PSM	SVSFDSLF	626	8		1926
PSA	SVTWIGAAPL	7	10		1927
PSA	SVTWIGAAPLI	7	11		1928

Table X

Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acid	A*2401	Seq. Id. No.
PSM	SVYETYEL	554	8		1929
PAP	SWATEDTM	225	8		1930
PAP	SWATEDTMTKL	225	11		1931
PAP	SWDAEEFGL	420	9		1932
PSM	SWDAEEFGLL	420	10		1933
PSM	SWGPEPCAL	228	9	0.0001	1934
Kallikrein	SWGSEPCAL	224	9	0.0013	1935
PSA	SWPQGFGQL	62	9		1936
PAP	SWRGSLKVPY	318	10		1937
PSM	SWTKKSPSPEF	496	11		1938
PSM	SYKHEQVY	96	8	0.2600	1939
PAP	SYKHEQVYI	96	9		1940
PAP	SYKKLIMY	279	8		1941
PAP	SYPDGWNL	241	8		1942
PSM	SYPNKTHPNY	118	10		1943
PSM	SYPNKTHPNYI	118	11		1944
PSM	TLGKLSGL	190	8		1945
PAP	TLKSEEFQKRL	171	11		1946
PAP	TLMSAMTNL	112	9		1947
PAP	TLPSWATEDTM	222	11		1948
PAP	TLRGAVEPDRY	361	11		1949
PSM	TLRVDCTPL	461	9		1950
PSM	TLRVDCTPLM	461	10		1951
PSM	TLRVDCTPLMY	461	11		1952
PSM	TMTKLREL	231	8		1953
PAP	TMTKLRELSEL	231	11		1954
PAP	TTCYASGW	150	8		1955
Kallikrein	TTCYASGW	146	8		1956
PSA	TTCYASGWGSI	150	11		1957
Kallikrein	TTCYASGWGSI	146	11		1958
PSA	TTVSGLQM	291	8		1959
PAP	TTVSGLQMAL	291	10		1960
PAP	TVAQVRGGM	575	9		1961
PSM	TVAQVRGGMVF	575	11		1962
PSM	TVPLSEDQL	145	9		1963
PAP	TVPLSEDQLL	145	10		1964
PAP	TVPLSEDQLLY	145	11		1965
PAP	TVQAAAETL	738	9		1966
PSM	TVSGLQMAL	292	9		1967
PAP	TWIGAAPL	9	8		1968
PSA	TWIGAAPLI	9	9	0.1100	1969
PSA	TWIGAAPLIL	9	9	0.3600	1970
PSA	TYELVEKF	558	10		1971
PSM	TYELVEKFY	558	8		1972
PSM	TYSVSFDSL	624	9		1973
PSM	TYSVSFDSLF	624	9		1974
PSM			10	3.2000	

Table X

Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Aci	A*2401	Seq. Id. No.
PSM	VFELANSI	584	8		1975
PSM	VFELANSIVL	584	10		1976
PSM	VFFQRLGI	523	8		1977
PSA	VFLTLSVTW	2	9	2.1000	1978
PSA	VFLTLSVTWI	2	10	0.0062	1979
PSA	VFQVSHSF	85	8		1980
PAP	VFRHGDRSPI	41	10	0.0005	1981
PSM	VIARYGKVF	201	9		1982
PSM	VILGGHRDSW	372	10		1983
PSA	VILLGRHSL	68	9		1984
PSA	VILLGRHSLF	68	10		1985
PSM	VILYSDPADY	225	10		1986
PSM	VILYSDPADYF	225	11		1987
PAP	VIPQDWSTECM	363	11		1988
PSM	VIYAPSSHNKY	690	11		1989
PSM	VLAGGFFL	27	8		1990
PSM	VLAGGFFLL	27	9		1991
PSM	VLAGGFFLLGF	27	11		1992
PAP	VLAKELKF	30	8		1993
PAP	VLAKELKFVTL	30	11		1994
Kallikrein	VLGLPTQEPAL	138	11		1995
PSM	VLPFDCRDY	592	9		1996
Kallikrein	VLQGITSW	222	8		1997
PSA	VLQGITSW	218	8		1998
PSM	VLRKYADKI	603	9		1999
PSM	VLRKYADKIY	603	10		2000
PSM	VLRMMNDQL	660	9		2001
PSM	VLRMMNDQLM	660	10		2002
PSM	VLRMMNDQLMF	660	11		2003
PSA	VLTAAHCI	56	8		2004
Kallikrein	VLTAAHCL	60	8		2005
Kallikrein	VLVHPQWVL	53	9		2006
PSA	VLVNEILNHM	49	9		2007
PAP	VMDLPTQEPAL	262	10		2008
PSA	VTEFMLCAGL	134	11		2009
Kallikrein	VTEFMLCAGLW	192	10		2010
Kallikrein	VTKFMLCAGRW	192	11		2011
PSA	VTRIYNVI	188	11		2012
PSM	VTRIYNVIGTL	352	8		2013
PSM	VTWIGAAPL	352	11		2014
PSA	VTWIGAAPLI	8	9		2015
PSA	VTWIGAAPLIL	8	10		2016
PSA	VVFLTLSVTW	8	11		2017
PSA	VVFLTLSVTWI	1	10		2018
PSM	VVHEIVRSF	1	11		2019
		394	9		2020

Table X

Prostate A24 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Aci...	A*2401	Seq. Id. No.
Kallikrein	VVIIYRKWI	246	8		2021
PSA	VVIIYRKWI	242	8		2022
PSM	VVLRKYADKI	602	10		2023
PSM	VVLRKYADKIY	602	11		2024
Kallikrein	VWLGRIINL	73	8		2025
Kallikrein	VWLGRIINLF	73	9		2026
PSM	VYETYELVEKF	555	11		2027
PAP	VYNGLLPPY	302	9	0.0320	2028
Kallikrein	VYTKVVIIY	242	8		2029
Kallikrein	VYTKVVIIYRKW	242	11		2030
PSM	VYVNYARTEDF	175	11		2031
PSA	WIGAAPLI	10	8		2032
PSA	WIGAAPLIL	10	9		2033
PSM	WLCAGALVL	20	9		2034
PAP	WLDRSVLAKEL	25	11		2035
Kallikrein	WLGRIINLF	74	8		2036
PSM	WTKKSPSPEF	497	10		2037
PSA	WVLTAAHCI	55	9		2038
Kallikrein	WVLTAAHCL	59	9		2039
PSM	YFAPGVKSY	234	9		2040
PAP	YFEKGEYF	319	8		2041
PAP	YFEKGEYFVEM	319	11		2042
PSM	YINADSSI	449	8		2043
PAP	YIRKRYRKF	84	9		2044
PAP	YIRKRYRKFL	84	10		2045
PAP	YIRSTDVDRTL	103	11		2046
PAP	YLPERNCPRF	155	10		2047
PSM	YTKNWETNKF	537	10		2048
Kallikrein	YTKVVIIYRKW	243	10		2049
PSA	YTKVVIIYRKW	239	10		2050
Kallikrein	YTKVVIIYRKWI	243	11		2051
PSA	YTKVVIIYRKWI	239	11		2052
PSM	YTLRVDCTPL	460	10		2053
PSM	YTLRVDCTPLM	460	11		2054
PSM	YVILGGHRDSW	371	11		2055
PSM	YVNYARTEDF	176	10		2056
PSM	YVNYARTEDFF	176	11		2057
PSM	YYDAQKLL	299	8		2058
PSM	YYDAQKLLEKM	299	11		2059
PAP	YYRNETQHEPY	330	11		2060

Table XI

Prostate B07 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	B*0702	Seq. Id. No.
PSM	APGVKSYPDGW	236	11		2061
PSA	APLILSRI	14	8		2062
PSA	APLILSRIV	14	9	0.0007	2063
PAP	APLLLARA	4	8		2064
PAP	APLLLARAA	4	9	0.0210	2065
PAP	APLLLARAASL	4	11		2066
PSM	APPDSSWRGSL	313	11		2067
PSM	APSSHNKY	693	8		2068
PSM	APSSHNKYA	693	9	0.0003	2069
PAP	CPLERFAEL	351	9	0.0810	2070
PAP	CPLERFAELV	351	10	0.0054	2071
PSM	DPADYFAPGV	230	10	0.0002	2072
PAP	DPIKESSW	56	8		2073
PSM	DPLGLPDRPF	677	10	0.0001	2074
PSM	DPLGLPDRPFY	677	11		2075
PSM	DPLTPGYPA	266	9	0.0001	2076
PAP	DPLYCESV	211	8		2077
PAP	DPLYCESVHNF	211	11		2078
PSM	DPMFKYHL	567	8		2079
PSM	DPMFKYHLTV	567	10	0.0001	2080
PSM	DPMFKYHLTVA	567	11		2081
PSM	DPQSGAAV	387	8		2082
PSM	DPQSGAAVV	387	9	0.0011	2083
PSM	DPSKAWGEV	720	9	0.0002	2084
PSA	EPAELTDA	124	8		2085
PSA	EPAELTDAV	124	9	0.0001	2086
PSA	EPAELTDAVKV	124	11		2087
Kallikrein	EPAKITDV	128	8		2088
Kallikrein	EPAKITDVV	128	9		2089
Kallikrein	EPAKITDVVKV	128	11		2090
Kallikrein	EPALGTTCY	145	9		2091
PSA	EPALGTTCY	141	9		2092
Kallikrein	EPALGTTCYA	145	10	0.0002	2093
PSA	EPALGTTCYA	141	10	0.0002	2094
Kallikrein	EPCALPEKPA	232	10		2095
Kallikrein	EPCALPEKPAV	232	11		2096
PSA	EPCALPERPSL	228	11		2097
PSM	EPDRYVIL	367	8		2098
Kallikrein	EPEDTGQRV	82	9		2099
Kallikrein	EPEDTGQRVPV	82	11		2100
Kallikrein	EPEEFLRPRSL	161	11		2101
PSA	EPEEFLTPKKL	157	11		2102
PSM	EPPPPGYENV	145	10	0.0001	2103
PSM	FPGIYDAL	705	8		2104
PSM	FPGIYDALF	705	9	0.0013	2105
PSM	FPGIYDALFDI	705	11		2106

Table XI

Prostate B07 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	B*0702	Seq. Id. No.
PSA	FPHPLYDM	92	8		2107
PSA	FPHPLYDMSL	92	10	1.1000	2108
PSA	FPHPLYDMSLL	92	11		2109
Kallikrein	FPHPLYNM	96	8		2110
Kallikrein	FPHPLYNMSL	96	10		2111
Kallikrein	FPHPLYNMSLL	96	11		2112
PAP	FPPEGVSI	124	8		2113
PAP	FPPEGVSIW	124	9	0.0001	2114
PAP	FPTDPIKESSW	53	11		2115
PSM	GPGFTGNF	330	8		2116
Kallikrein	GPLVCNGV	215	8		2117
PSA	GPLVCNGV	211	8		2118
Kallikrein	GPLVCNGVL	215	9	0.0280	2119
PSA	GPLVCNGVL	211	9	0.0280	2120
PAP	GPVIPQDW	361	8		2121
PSA	HPEDTGQV	78	8		2122
PSA	HPEDTGQVF	78	9	0.0006	2123
PSA	HPEDTGQVFQV	78	11		2124
PSM	HPIGYYDA	295	8		2125
PSM	HPIGYYDAQKL	295	11		2126
PSA	HPLYDMSL	94	8		2127
PSA	HPLYDMSLL	94	9	0.0018	2128
Kallikrein	HPLYNMSL	98	8		2129
Kallikrein	HPLYNMSLL	98	9		2130
PSM	HPNYISIL	124	8		2131
PSM	HPQEMKTY	618	8		2132
PSM	HPQEMKTYSV	618	10	0.0003	2133
PSA	HPQKVTKF	184	8		2134
PSA	HPQKVTKFM	184	9	0.1700	2135
PSA	HPQKVTKFML	184	10	0.0230	2136
Kallikrein	HPQWVLTA	56	8		2137
PSA	HPQWVLTA	52	8		2138
Kallikrein	HPQWVLTAA	56	9	0.0240	2139
PSA	HPQWVLTAA	52	9	0.0240	2140
PAP	HPYKDFIA	182	8		2141
PAP	HPYKDFIATL	182	10	0.0150	2142
PSM	IPHLAGTEQNF	80	11		2143
PAP	IPQDWSTECM	364	10	0.0019	2144
PAP	IPSYKKLI	277	8		2145
PAP	IPSYKKLIM	277	9	5.8000	2146
PAP	IPSYKKLIMY	277	10		2147
PSM	IPVIIPIGY	292	8		2148
PSM	IPVIIPIGYY	292	9	0.0007	2149
PSM	IPVIIPIGYYDA	292	11		2150
PAP	IPVHTVPL	141	8		2151
Kallikrein	KPAVYTKV	239	8		2152

Table XI

Prostate B07-Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	B*0702	Seq. Id. No.
Kallikrein	KPAVYTKVV	239	9		2153
Kallikrein	KPAVYTKVVHY	239	11		2154
PSM	LPDRPFYRHV	681	10	0.0007	2155
PSM	LPDRPFYRHVI	681	11		2156
Kallikrein	LPEKPAVY	236	8		2157
Kallikrein	LPEKPAVYTKV	236	11		2158
PSA	LPERPSLY	232	8		2159
PSA	LPERPSLYTKV	232	11		2160
PSM	LPFDCRDY	593	8		2161
PSM	LPFDCRDYA	593	9	0.0011	2162
PSM	LPFDCRDYAV	593	10	0.0150	2163
PSM	LPFDCRDYAVV	593	11		2164
PAP	LPFRNCPRF	156	9	0.0049	2165
PAP	LPGCSPSCPL	344	10	0.0360	2166
PSM	LPGGGVQRGNI	248	11		2167
PAP	LPPYASCHL	307	9	0.0029	2168
PSM	LPSIPVHPI	289	9	0.0790	2169
PSM	LPSIPVHPIGY	289	11		2170
PAP	LPSWATEDTM	223	10	0.0032	2171
Kallikrein	LPTQEPAL	141	8		2172
PSA	LPTQEPAL	137	8		2173
PSM	MPEGDLVY	169	8		2174
PSM	MPEGDLVYV	169	9	0.0001	2175
PSM	MPEGDLVYVNY	169	11		2176
PAP	NPILLWQPI	133	9	0.0026	2177
PAP	NPILLWQPIPV	133	11		2178
PSM	NPIVLRMM	657	8		2179
PSM	PPDSSWRGSL	314	10	0.0012	2180
PAP	PPEGVSIW	125	8		2181
PAP	PPEGVSIWNPI	125	11		2182
PSM	PPESAFSPQGM	159	11		2183
PSM	PPGYENVSDI	148	10	0.0001	2184
PSM	PPGYENVSDIV	148	11		2185
PSM	PPPGYENV	147	8		2186
PSM	PPPGYENVSDI	147	11		2187
PSM	PPPPGYENV	146	9	0.0001	2188
PAP	PPYASCHL	308	8		2189
PAP	PPYASCHLTEL	308	11		2190
PAP	QPIPVHTV	139	8		2191
PAP	QPIPVHTVPL	139	10	0.2400	2192
Kallikrein	QPWQVAVY	36	8		2193
PSA	QPWQVLVA	32	8		2194
Kallikrein	RPDEDSSHDL	112	10		2195
Kallikrein	RPDEDSSHDLM	112	11		2196
PSM	RPFYRHVI	684	8		2197
PSM	RPFYRHVIY	684	9	0.4700	2198

Table XI

Prostate 007 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	B*0702	Seq. Id. No.
PSM	RPFYRHVIYA	684	10	0.7200	2199
PSA	RPGDDSSHDL	108	10	0.0117	2200
PSA	RPGDDSSHDLM	108	11		2201
PSM	RPRRTILF	411	8		2202
PSM	RPRRTILFA	411	9	0.7800	2203
PSM	RPRRTILFASW	411	11		2204
Kallikrein	RPRSLQCV	167	8		2205
Kallikrein	RPRSLQCVSL	167	10		2206
PSM	RPRWLCAGA	17	9	0.3200	2207
PSM	RPRWLCAGAL	17	10	5.2000	2208
PSM	RPRWLCAGALV	17	11		2209
PSA	RPSLYTKV	235	8		2210
PSA	RPSLYTKVV	235	9		2211
PSA	RPSLYTKVVHY	235	11		2212
PSM	SPDEGFEGKSL	483	11		2213
PSM	SPEFSGMPRI	503	10	0.0020	2214
PAP	SPIDTEPTDPI	48	11		2215
PSM	SPQGMPEGDL	165	10	0.0002	2216
PSM	SPQGMPEGDLV	165	11		2217
PAP	SPSCPLERF	348	9	0.0066	2218
PAP	SPSCPLERFA	348	10	0.0002	2219
PSM	SPSPEFSGM	501	9	0.0025	2220
PSM	TPGYPANEY	269	9	0.0012	2221
PSM	TPGYPANEYA	269	10	0.0001	2222
PSM	TPGYPANEYAY	269	11		2223
PSM	TPKHNMKA	53	8		2224
PSM	TPKHNMKAF	53	9	0.0990	2225
PSM	TPKHNMKAFL	53	10	0.0200	2226
PSA	TPKKLQCV	163	8		2227
PSA	TPKKLQCVDL	163	10	0.0006	2228
PSM	TPLMYSLV	467	8		2229
PSM	TPLMYSLVHNL	467	11		2230
Kallikrein	VPLIQSRI	18	8		2231
Kallikrein	VPLIQSRIV	18	9		2232
PAP	VPLSEDQL	146	8		2233
PAP	VPLSEDQLL	146	9	0.0002	2234
PAP	VPLSEDQLLY	146	10	0.0011	2235
PAP	VPLSEDQLLYL	146	11		2236
Kallikrein	VPVSHSFPHPL	90	11		2237
PSM	VPYNVGPGF	325	9	0.0039	2238
PAP	WPQGFGQL	63	8		2239
PAP	WPQGFGQLTQL	63	11		2240
PSM	YPANEYAY	272	8		2241
PSM	YPLYHSVY	549	8		2242
PSM	YPLYHSVYETY	549	11		2243
PSM	YPNKTHPNY	119	9	0.0001	2244

Table XI

Prostate B07 Supermotif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	B*0702	Seq. Id. No.
PSM	YPNKTHPNYI	119	10	0.0035	2245

Table XII
Prostate B27 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
Kallikrein	AHCGGVLV	48	8	2246
PSA	AHCIRNKSV	60	9	2247
PSA	AHCIRNKSVI	60	10	2248
PSA	AHCIRNKSVIL	60	11	2249
Kallikrein	AHCLKKNSQV	64	10	2250
Kallikrein	AHCLKKNSQVW	64	11	2251
PAP	AHDTTVSGL	288	9	2252
PAP	AHDTTVSGLQM	288	11	2253
PSM	AHYDVLLSY	111	9	2254
PAP	AKELKFVTL	32	9	2255
PAP	AKELKFVTLV	32	10	2256
PAP	AKELKFVTLVF	32	11	2257
PSM	AKGVILYSDPA	222	11	2258
Kallikrein	AKITDVVKV	130	9	2259
Kallikrein	AKITDVVKVL	130	10	2260
PSM	AKQIQSQW	93	8	2261
PSM	AKQIQSQWKEF	93	11	2262
PAP	ARAASLSL	9	8	2263
PAP	ARAASLSLGF	9	10	2264
PAP	ARAASLSLGFL	9	11	2265
Kallikrein	ARAYSEKV	185	8	2266
Kallikrein	ARAYSEKVTEF	185	11	2267
PSM	ARRPRWLCA	15	9	2268
PSM	ARRPRWLCAGA	15	11	2269
PSM	ARTEDFFKL	180	9	2270
PAP	CHLTELYF	313	8	2271
PSM	CRDYAVVL	597	8	2272
PSM	CRDYAVVLRKY	597	11	2273
PSM	DKIYSISM	609	8	2274
PSM	DKSNPIVL	654	8	2275
PSM	DKSNPIVLRM	654	10	2276
PSM	DKSNPIVLRMM	654	11	2277
PSM	DRPFYRHV	683	8	2278
PSM	DRPFYRHVI	683	9	2279
PSM	DRPFYRHVIY	683	10	2280
PSM	DRPFYRHVIYA	683	11	2281
PAP	DRSPIDTF	46	8	2282
PAP	DRSVLAKEL	27	9	2283
PAP	DRSVLAKELKF	27	11	2284
PAP	DRTLMSAM	110	8	2285
PAP	DRTLMSAMTNL	110	11	2286
PSM	EKFYDPMF	563	8	2287
PSM	EKFYDPMFKY	563	10	2288
PAP	EKGEYFVEM	321	9	2289

Table XII
Prostate B27 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PAP	EKGEYFVEMY	321	10	2290
PAP	EKGEYFVEMYY	321	11	2291
Kallikrein	EKHSQPWQV	32	9	2292
PSA	EKHSQPWQV	28	9	2293
Kallikrein	EKHSQPWQVA	32	10	2294
Kallikrein	EKHSQPWQVAV	32	11	2295
PSA	EKHSQPWQVL	28	10	2296
PSA	EKHSQPWQVLV	28	11	2297
Kallikrein	EKPAVYTKV	238	9	2298
Kallikrein	EKPAVYTKVV	238	10	2299
PAP	EKSRLQGGV	254	9	2300
PAP	EKSRLQGGVL	254	10	2301
PAP	EKSRLQGGVLV	254	11	2302
Kallikrein	EKVTEFML	190	8	2303
Kallikrein	EKVTEFMLCA	190	10	2304
PSM	ERAFIDPL	672	8	2305
PSM	ERAFIDPLGL	672	10	2306
PAP	ERFAELVGPV	354	10	2307
PAP	ERFAELVGPVI	354	11	2308
PSM	ERGVAYINA	444	9	2309
PSA	ERPSLYTKV	234	9	2310
PSA	ERPSLYTKVV	234	10	2311
PSA	FHPEDTGQV	77	9	2312
PSA	FHPEDTGQVF	77	10	2313
PSM	FKLERDMKI	186	9	2314
PSM	FKYHLTVA	570	8	2315
PSM	FKYHLTVAQV	570	10	2316
PSM	FRGNKVKNA	209	9	2317
PSM	FRGNKVKNAQL	209	11	2318
PAP	FRHGDRSPI	42	9	2319
PAP	FRNCPRFQEL	158	10	2320
PSM	GHRDSWVF	376	8	2321
PSM	GHRDSWVFGGI	376	11	2322
PSM	GKIVIARY	198	8	2323
PSM	GKIVIARYGKV	198	11	2324
PAP	GKLSGLHGQDL	192	11	2325
PSM	GKSLYESW	490	8	2326
PSM	GKVFRGNKV	206	9	2327
PSM	GRARYTKNW	533	9	2328
PSA	GRAVCGGV	42	8	2329
PSA	GRAVCGGVL	42	9	2330
PSA	GRAVCGGVLV	42	10	2331
PAP	HKQKEKSRL	250	9	2332
PSM	HRDSWVFGGI	377	10	2333

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Prostate 127 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PAP	IHKQKEKSRL	249	10	2334
PSM	IHSTNEVTRI	346	10	2335
PSM	IHSTNEVTRIY	346	11	2336
PAP	IKESSWPQGF	58	10	2337
PSM	IKKFLYNF	70	8	2338
PSM	IKKFLYNFTQI	70	11	2339
PSM	IKSSNEATNI	43	10	2340
PAP	IRKRYRKF	85	8	2341
PAP	IRKRYRKFL	85	9	2342
PSA	IRNKSVIL	63	8	2343
PSA	IRNKSVILL	63	9	2344
PAP	IRSTDVDRTL	104	10	2345
PAP	IRSTDVDRTLM	104	11	2346
PSM	KHNMKAFL	55	8	2347
PSM	KHNMKAFLDEL	55	11	2348
PSM	KHPQEMKTY	617	9	2349
PSM	KHPQEMKTYSV	617	11	2350
Kallikrein	KHSQPWQV	33	8	2351
PSA	KHSQPWQV	29	8	2352
Kallikrein	KHSQPWQVA	33	9	2353
Kallikrein	KHSQPWQVAV	33	10	2354
Kallikrein	KHSQPWQVAVY	33	11	2355
PSA	KHSQPWQVL	29	9	2356
PSA	KHSQPWQVLV	29	10	2357
PSA	KHSQPWQVLVA	29	11	2358
PSM	KKEGWRPRRTI	406	11	2359
PSM	KKFLYNFTQI	71	10	2360
PAP	KKLIMYSA	281	8	2361
PSA	KKLQCVDL	165	8	2362
PSA	KKLQCVDLHV	165	10	2363
PSA	KKLQCVDLHVI	165	11	2364
Kallikrein	KKNSQVWL	68	8	2365
PSM	KKSPSPEF	499	8	2366
PSM	KKSPSPEFSGM	499	11	2367
PAP	KRATQIPSY	272	9	2368
PAP	KRLHPYKDF	179	9	2369
PAP	KRLHPYKDFI	179	10	2370
PAP	KRLHPYKDFIA	179	11	2371
PSM	KRQIYVAA	729	8	2372
PSM	KRQIYVAAF	729	9	2373
PSM	KRQIYVAAFTV	729	11	2374
PAP	KRYRKFLNESY	87	11	2375
PSM	LHETDSAV	5	8	2376
PSM	LHETDSAVA	5	9	2377

Table XII
Prostate B27 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	LHETDSAVATA	5	11	2378
PAP	LHGQDLFGI	197	9	2379
PAP	LHGQDLFGIW	197	10	2380
Kallikrein	LHLLSNDM	176	8	2381
Kallikrein	LHLLSNDMCA	176	10	2382
PAP	LHPYKDFI	181	8	2383
PAP	LHPYKDFIA	181	9	2384
PAP	LHPYKDFIATL	181	11	2385
PSA	LHVISNDV	172	8	2386
PSA	LHVISNDVCA	172	10	2387
PSM	LKAENIKKF	65	9	2388
PSM	LKAENIKKFL	65	10	2389
PSM	LKAENIKKFLY	65	11	2390
PAP	LKFVTLVF	35	8	2391
Kallikrein	LKKNSQVW	67	8	2392
Kallikrein	LKKNSQVWL	67	9	2393
PAP	LKSEEFQKRL	172	10	2394
PSM	LKSPDEGF	481	8	2395
PSM	LKVPYNVGPGF	323	11	2396
PAP	LRELSELSL	235	9	2397
PAP	LRELSELSLL	235	10	2398
PSM	LRGAVEPDRY	362	10	2399
PSM	LRGAVEPDRYV	362	11	2400
PSM	LRKYADKI	604	8	2401
PSM	LRKYADKIY	604	9	2402
PSM	LRKYADKIYSI	604	11	2403
PSA	LRLSEPAEL	120	9	2404
Kallikrein	LRLSEPAKI	124	9	2405
PSM	LRMMNDQL	661	8	2406
PSM	LRMMNDQLM	661	9	2407
PSM	LRMMNDQLMF	661	10	2408
PSM	LRMMNDQLMFL	661	11	2409
Kallikrein	LRPDEDSSHDL	111	11	2410
PSA	LRPGDDSSHDL	107	11	2411
Kallikrein	LRPRSLQCV	166	9	2412
Kallikrein	LRPRSLQCVSL	166	11	2413
PSM	LRVDCTPL	462	8	2414
PSM	LRVDCTPLM	462	9	2415
PSM	LRVDCTPLMY	462	10	2416
PSM	MHIHSTNEV	344	9	2417
PSM	MKAFLDEL	58	8	2418
PSM	MKAFLDELKA	58	10	2419
PSM	MKHPQEMKTY	616	10	2420
PSM	MKINCSGKI	192	9	2421

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Prostate 32 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	MKINCSGKIV	192	10	2422
PSM	MKINCSGKIVI	192	11	2423
PAP	MKRATQIPSY	271	10	2424
PSM	MKTYSVSF	622	8	2425
PSM	MKTYSVSFDSL	622	11	2426
PAP	MRAAPLLL	1	8	2427
PAP	MRAAPLLLA	1	9	2428
PAP	MRAAPLLLARA	1	11	2429
PAP	NHMKRATQI	269	9	2430
PSM	NKFSGYPL	544	8	2431
PSM	NKFSGYPLY	544	9	2432
PSM	NKTHPNYI	121	8	2433
PSM	NKTHPNYISI	121	10	2434
PSM	NKTHPNYISII	121	11	2435
PSM	NKVKNAQL	212	8	2436
PSM	NKVKNAQLA	212	9	2437
PSM	NKVKNAQLAGA	212	11	2438
PSM	NKYAGESF	698	8	2439
PSM	NKYAGESFPGI	698	11	2440
PSM	PHLAGTEQNF	81	10	2441
PSA	PHPLYDMSL	93	9	2442
PSA	PHPLYDMSLL	93	10	2443
Kallikrein	PHPLYNMSL	97	9	2444
Kallikrein	PHPLYNMSLL	97	10	2445
PSM	PKHNMKAF	54	8	2446
PSM	PKHNMKAFL	54	9	2447
PSA	PKKLQCVDL	164	9	2448
PSA	PKKLQCVDLHV	164	11	2449
PAP	PRFQELESETL	162	11	2450
PSM	PRRTILFA	412	8	2451
PSM	PRRTILFASW	412	10	2452
Kallikrein	PRSLQCVSL	168	9	2453
Kallikrein	PRSLQCVSLHL	168	11	2454
PSM	PRWLCAGA	18	8	2455
PSM	PRWLCAGAL	18	9	2456
PSM	PRWLCAGALV	18	10	2457
PSM	PRWLCAGALVL	18	11	2458
PAP	QHEPYPLM	336	8	2459
PAP	QHEPYPLML	336	9	2460
PAP	QHYELGEY	77	8	2461
PAP	QHYELGEYI	77	9	2462
PAP	QKEKSRLQGGV	252	11	2463
PSM	QKLLEKMGGSA	303	11	2464
PAP	QKRLHPYKDF	178	10	2465

Table XII

Prostate B27 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PAP	QKRLHPYKDFI	178	11	2466
PSA	QKVTKFML	186	8	2467
PSA	QKVTKFMLCA	186	10	2468
PSM	QRGNILNL	254	8	2469
PSM	QRGNILNLNGA	254	11	2470
PSM	QRLGIASGRA	526	10	2471
Kallikrein	QRVPVSHSF	88	9	2472
PAP	RHGDRSPI	43	8	2473
PAP	RHGDRSPIDTF	43	11	2474
PAP	RKFLNESY	90	8	2475
PAP	RKRYRKFL	86	8	2476
Kallikrein	RKWIKDTI	250	8	2477
PSA	RKWIKDTI	246	8	2478
Kallikrein	RKWIKDTIA	250	9	2479
Kallikrein	RKWIKDTIAA	250	10	2480
PSA	RKWIKDTIV	246	9	2481
PSA	RKWIKDTIVA	246	10	2482
PSM	RKYADKIY	605	8	2483
PSM	RKYADKIYSI	605	10	2484
PSM	RRGIAEAV	280	8	2485
PSM	RRGIAEAVGL	280	10	2486
PSM	RRPRWLCA	16	8	2487
PSM	RRPRWLCAGA	16	10	2488
PSM	RRPRWLCAGAL	16	11	2489
PSM	RRTILFASW	413	9	2490
PSM	RRTILFASWDA	413	11	2491
Kallikrein	SHDLMLLRL	118	9	2492
PSA	SHDLMLLRL	114	9	2493
Kallikrein	SHGWAHCGGV	44	10	2494
Kallikrein	SHGWAHCGGVL	44	11	2495
PSM	SHNKYAGESF	696	10	2496
Kallikrein	SHSFPHPL	93	8	2497
PSA	SHSFPHPL	89	8	2498
Kallikrein	SHSFPHPLY	93	9	2499
PSA	SHSFPHPLY	89	9	2500
PSA	SHSFPHPLYDM	89	11	2501
Kallikrein	SHSFPHPLYNM	93	11	2502
PSM	SKAWGEVKRQI	722	11	2503
PSM	SKFSERLQDF	644	10	2504
PSM	SKLGSGNDF	513	9	2505
PSM	SKLGSGNDFEV	513	11	2506
PSM	SKVDPSKA	717	8	2507
PSM	SKVDPSKAW	717	9	2508
PAP	SKVYDPLY	207	8	2509

Table XII
Prostate B27 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSA	SRGRAVCGGV	40	10	2510
PSA	SRGRAVCGGVL	40	11	2511
PSM	SRLLQERGV	439	9	2512
PSM	SRLLQERGVA	439	10	2513
PSM	SRLLQERGVAY	439	11	2514
PAP	SRLQGGVL	256	8	2515
PAP	SRLQGGVLV	256	9	2516
PSM	THPNYISI	123	8	2517
PSM	THPNYISII	123	9	2518
PSM	TKELKSPDEGF	478	11	2519
PSA	TKFMLCAGRW	189	10	2520
PSM	TKKSPSPEF	498	9	2521
PAP	TKLRELSEL	233	9	2522
PAP	TKLRELSELSL	233	11	2523
PSM	TKNWETNKF	538	9	2524
Kallikrein	TKVVHYRKW	244	9	2525
PSA	TKVVHYRKW	240	9	2526
Kallikrein	TKVVHYRKWI	244	10	2527
PSA	TKVVHYRKWI	240	10	2528
PSM	TRIYNVIGTL	353	10	2529
PSM	VHEIVRSF	395	8	2530
PSM	VHEIVRSFGTL	395	11	2531
PAP	VHNFTLPSW	218	9	2532
PAP	VHNFTLPSWA	218	10	2533
PSM	VHNLTKEL	474	8	2534
PSM	VHPIGYYDA	294	9	2535
PSA	VHPQKVTKF	183	9	2536
PSA	VHPQKVTKFM	183	10	2537
PSA	VHPQKVTKFML	183	11	2538
Kallikrein	VHPQWVLTA	55	9	2539
PSA	VHPQWVLTA	51	9	2540
Kallikrein	VHPQWVLTAA	55	10	2541
PSA	VHPQWVLTAA	51	10	2542
PAP	VHTVPLSEDQL	143	11	2543
Kallikrein	VHYRKWIKDTI	247	11	2544
PSA	VHYRKWIKDTI	243	11	2545
PSM	VKMHIHSTNEV	342	11	2546
PSM	VKNAQLAGA	214	9	2547
PSM	VKNFTEIA	636	8	2548
PSM	VKNFTEIASKF	636	11	2549
PSM	VKRQIYVA	728	8	2550
PSM	VKRQIYVAA	728	9	2551
PSM	VKRQIYVAAF	728	10	2552
PSM	VKSYPDGW	239	8	2553

Table XII
Prostate B27 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	VKSYPDGWNL	239	10	2554
PSM	VRGGMVFEL	579	9	2555
PSM	VRGGMVFELA	579	10	2556
PSM	WKEFGLDSV	100	9	2557
PSM	WKEFGLDSVEL	100	11	2558
PSM	WRGSLKVPY	319	9	2559
PSM	WRGSLKVPYNV	319	11	2560
PSM	WRPRRTIL	410	8	2561
PSM	WRPRRTILF	410	9	2562
PSM	WRPRRTILFA	410	10	2563
PSM	YHLTVAQV	572	8	2564
PSM	YHSVYETY	552	8	2565
PSM	YHSVYETYEL	552	10	2566
PSM	YHSVYETYELV	552	11	2567
PAP	YKDFIATL	184	8	2568
PAP	YKDFIATLGKL	184	11	2569
PAP	YKHEQVYI	97	8	2570
PAP	YKKLIMYSA	280	9	2571
PAP	YRKFLNESY	89	9	2572
Kallikrein	YRKWIKDTI	249	9	2573
PSA	YRKWIKDTI	245	9	2574
Kallikrein	YRKWIKDTIA	249	10	2575
Kallikrein	YRKWIKDTIAA	249	11	2576
PSA	YRKWIKDTIV	245	10	2577
PSA	YRKWIKDTIVA	245	11	2578
PAP	YRNETQHEPY	331	10	2579
PSM	YRRGIAEA	279	8	2580
PSM	YRRGIAEAV	279	9	2581
PSM	YRRGIAEAVGL	279	11	2582

Table XIII

Prostate B58 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	AAAETLSEV	741	9	2583
PSM	AAAETLSEVA	741	10	2584
PSM	AAETLSEV	742	8	2585
PSM	AAETLSEVA	742	9	2586
PSM	AAFTVQAA	735	8	2587
PSM	AAFTVQAAA	735	9	2588
PSA	AAHCIRNKSV	59	10	2589
PSA	AAHCIRNKSVI	59	11	2590
Kallikrein	AAHCLKKNSQV	63	11	2591
PAP	AALFPPEGV	121	9	2592
PAP	AALFPPEGVSI	121	11	2593
PSA	AAPLILSRI	13	9	2594
PSA	AAPLILSRIV	13	10	2595
PAP	AAPLLLARA	3	9	2596
PAP	AAPLLLARAA	3	10	2597
PAP	AASLSLGF	11	8	2598
PAP	AASLSLGFL	11	9	2599
PAP	AASLSLGFLF	11	10	2600
PAP	AASLSLGFLFL	11	11	2601
PSM	AAVVHEIV	392	8	2602
PSM	AAVVHEIVRSF	392	11	2603
PAP	ASCHLTEL	311	8	2604
PAP	ASCHLTELY	311	9	2605
PAP	ASCHLTELYF	311	10	2606
PSM	ASGRARYTKNW	531	11	2607
PSM	ASKFSERL	643	8	2608
PSM	ASKFSERLQDF	643	11	2609
PAP	ASLSLGFL	12	8	2610
PAP	ASLSLGFLF	12	9	2611
PAP	ASLSLGFLFL	12	10	2612
PAP	ASLSLGFLFLL	12	11	2613
PSA	ASRGRAVCGGV	39	11	2614
PSM	ASWDAEEF	419	8	2615
PSM	ASWDAEEFGL	419	10	2616
PSM	ASWDAEEFGLL	419	11	2617
PSM	ATARRPRW	13	8	2618
PSM	ATARRPRWL	13	9	2619
PSM	ATARRPRWLCA	13	11	2620
PAP	ATEDTMTKL	227	9	2621
PAP	ATLGKLSGL	189	9	2622
PSM	ATNITPKHNM	49	10	2623
PAP	ATQIPSYKKL	274	10	2624
PAP	ATQIPSYKKLI	274	11	2625
PSM	CAGALVLA	22	8	2626

Table XIII
Prostate B58 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	CAGALVLAGGF	22	11	2627
Kallikrein	CALPEKPA	234	8	2628
Kallikrein	CALPEKPAV	234	9	2629
Kallikrein	CALPEKPAVY	234	10	2630
PSA	CALPERPSL	230	9	2631
PSA	CALPERPSLY	230	10	2632
PSA	CAQVHPQKV	180	9	2633
Kallikrein	CARAYSEKV	184	9	2634
PSA	CSGDSGGPL	205	9	2635
PSA	CSGDSGGPLV	205	10	2636
PSM	CSGKIVIA	196	8	2637
PSM	CSGKIVIARY	196	10	2638
PAP	CSPSCPLERF	347	10	2639
PAP	CSPSCPLERFA	347	11	2640
Kallikrein	CTGAVPLI	14	8	2641
PSM	CTPLMYSL	466	8	2642
PSM	CTPLMYSLV	466	9	2643
PSM	DAEEFGLL	422	8	2644
PSM	DALFDIESKV	710	10	2645
PSM	DAQKLLEKM	301	9	2646
PSA	DAVKVMDL	130	8	2647
Kallikrein	DSGGPLVCNGV	212	11	2648
PSA	DSGGPLVCNGV	208	11	2649
PSM	DSLFSAVKNF	630	10	2650
Kallikrein	DSSHDLML	116	8	2651
PSA	DSSHDLML	112	8	2652
Kallikrein	DSSHDLMLL	116	9	2653
PSA	DSSHDLMLL	112	9	2654
Kallikrein	DSSHDLMLLRL	116	11	2655
PSA	DSSHDLMLLRL	112	11	2656
PSM	DSSIEGNY	453	8	2657
PSM	DSSIEGNYTL	453	10	2658
PSM	DSSWRGSL	316	8	2659
PSM	DSSWRGSLKV	316	10	2660
PSM	DSVELAHY	106	8	2661
PSM	DSVELAHYDV	106	10	2662
PSM	DSVELAHYDVL	106	11	2663
PSM	DSWVFGGI	379	8	2664
Kallikrein	DTCGGDSGGPL	207	11	2665
PAP	DTFPTDPI	51	8	2666
Kallikrein	DTGQRVPV	85	8	2667
PSA	DTGQVFQV	81	8	2668
PAP	DTMTKLREL	230	9	2669
PAP	DTTVSGLQM	290	9	2670

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Prostate B58 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PAP	DTTVSGLQMA	290	10	2671
PAP	DTTVSGLQMAL	290	11	2672
PSM	EATNITPKHNM	48	11	2673
PSM	EAVGLPSI	285	8	2674
PSM	EAVGLPSIPV	285	10	2675
PAP	ESETLKSEEF	168	10	2676
PSM	ESFPGIYDA	703	9	2677
PSM	ESFPGIYDAL	703	10	2678
PSM	ESFPGIYDALF	703	11	2679
PSM	ESKVDPSKA	716	9	2680
PSM	ESKVDPSKAW	716	10	2681
PAP	ESSWPQGF	60	8	2682
PAP	ESSWPQGFGQL	60	11	2683
PAP	ESVHNFTL	216	8	2684
PAP	ESVHNFTLPSW	216	11	2685
PAP	ESYKHEQV	95	8	2686
PAP	ESYKHEQVY	95	9	2687
PAP	ESYKHEQVYI	95	10	2688
PSM	ETDSAVATA	7	9	2689
PAP	ETLKSEEF	170	8	2690
PSM	ETNKFSGY	542	8	2691
PSM	ETNKFSGYPL	542	10	2692
PSM	ETNKFSGYPLY	542	11	2693
PAP	ETQHEPYPL	334	9	2694
PAP	ETQHEPYPLM	334	10	2695
PAP	ETQHEPYPLML	334	11	2696
PSM	ETYELVEKF	557	9	2697
PSM	ETYELVEKFY	557	10	2698
PAP	FAELVGPV	356	8	2699
PAP	FAELVGPVI	356	9	2700
PSM	FAPGVKSY	235	8	2701
PSM	FASWDAEEF	418	9	2702
PSM	FASWDAEEFGL	418	11	2703
PSM	FSAFSPQGM	161	9	2704
PSM	FSAVKNFTEI	633	10	2705
PSM	FSAVKNFTEIA	633	11	2706
PSM	FSERLQDF	646	8	2707
PSM	FSGMPRISKL	506	10	2708
PSM	FSGYPLYHSV	546	10	2709
PSM	FSGYPLYHSVY	546	11	2710
PSM	FSPQGMPEGDL	164	11	2711
PSM	FSTQKVKM	337	8	2712
PSM	FSTQKVKMHI	337	10	2713
PSM	FTEIASKF	639	8	2714

Table XIII

Prostate B58 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	FTGNFSTQKV	333	10	2715
PSM	FTQIPHLA	77	8	2716
PSM	FTVQAAAETL	737	10	2717
PSA	GAAPLILSRI	12	10	2718
PSA	GAAPLILSRIV	12	11	2719
PSM	GAAVVHEI	391	8	2720
PSM	GAAVVHEIV	391	9	2721
PSM	GAGDPLTPGY	263	10	2722
PSM	GAKGVILY	221	8	2723
PSM	GALVLAGGF	24	9	2724
PSM	GALVLAGGFF	24	10	2725
PSM	GALVLAGGFFL	24	11	2726
PSM	GAVEPDRY	364	8	2727
PSM	GAVEPDRYV	364	9	2728
PSM	GAVEPDRYVI	364	10	2729
PSM	GAVEPDRYVIL	364	11	2730
Kallikrein	GAVPLIQSRI	16	10	2731
Kallikrein	GAVPLIQSRIV	16	11	2732
PSM	GSAPPDSSW	311	9	2733
PSM	GSGNDFEV	516	8	2734
PSM	GSGNDFEVF	516	9	2735
PSM	GSGNDFEVFF	516	10	2736
Kallikrein	GSIEPEEF	158	8	2737
PSA	GSIEPEEF	154	8	2738
Kallikrein	GSIEPEEFL	158	9	2739
PSA	GSIEPEEFL	154	9	2740
PSM	GSLKVPYNV	321	9	2741
PSM	GTEQNFQL	85	8	2742
PSM	GTEQNFQLA	85	9	2743
PSM	GTLKKEGW	403	8	2744
Kallikrein	GTTCYASGW	149	9	2745
PSA	GTTCYASGW	145	9	2746
Kallikrein	HSFPHPLY	94	8	2747
PSA	HSFPHPLY	90	8	2748
PSA	HSFPHPLYDM	90	10	2749
Kallikrein	HSFPHPLYNM	94	10	2750
Kallikrein	HSQPWQVA	34	8	2751
Kallikrein	HSQPWQVAV	34	9	2752
Kallikrein	HSQPWQVAVY	34	10	2753
PSA	HSQPWQVL	30	8	2754
PSA	HSQPWQVLV	30	9	2755
PSA	HSQPWQVLVA	30	10	2756
PSM	HSTNEVTRI	347	9	2757
PSM	HSTNEVTRIY	347	10	2758

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Prostate D58 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	HSVYETYEL	553	9	2759
PSM	HSVYETYELV	553	10	2760
PAP	HTVPLSEDQL	144	10	2761
PAP	HTVPLSEDQLL	144	11	2762
PSM	IAEAVGLPSI	283	10	2763
Kallikrein	IALSVGCTGA	8	10	2764
Kallikrein	IALSVGCTGAV	8	11	2765
PSM	IARYGKVF	202	8	2766
PSM	IASGRARY	530	8	2767
PSM	IASKFSERL	642	9	2768
PAP	IATLGKLSGL	188	10	2769
PSM	ISHNEDGNEI	128	11	2770
PSM	ISKLGSGNDF	512	10	2771
PSM	ISMKHPQEM	614	9	2772
PSA	ISNDVCAQV	175	9	2773
Kallikrein	ITDVVKVL	132	8	2774
Kallikrein	ITDVVKVLGL	132	10	2775
PSM	ITPKHNMKA	52	9	2776
PSM	ITPKHNMKAF	52	10	2777
PSM	ITPKHNMKAFL	52	11	2778
Kallikrein	ITSWGPEPCA	226	10	2779
Kallikrein	ITSWGPEPCAL	226	11	2780
PSA	ITSWGSEPCA	222	10	2781
PSA	ITSWGSEPCAL	222	11	2782
PSM	KAENIKKF	66	8	2783
PSM	KAENIKKFL	66	9	2784
PSM	KAENIKKFLY	66	10	2785
PSM	KAFLDELKA	59	9	2786
PSM	KAWGEVKRQI	723	10	2787
PSM	KAWGEVKRQIY	723	11	2788
PAP	KSEEFQKRL	173	9	2789
PSM	KSNPIVLRM	655	9	2790
PSM	KSNPIVLRMM	655	10	2791
PSM	KSPSPEFSGM	500	10	2792
PAP	KSRLQGGV	255	8	2793
PAP	KSRLQGGVL	255	9	2794
PAP	KSRLQGGVLV	255	10	2795
PSM	KSSNEATNI	44	9	2796
PSA	KSVILLGRHSL	66	11	2797
PSM	KSYPDGWNL	240	9	2798
PSM	KTHPNYISI	122	9	2799
PSM	KTHPNYISII	122	10	2800
PSM	KTYSVSFDSL	623	10	2801
PSM	KTYSVSFDSLF	623	11	2802

Table XIII

Prostate HLA Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PAP	LAALFPPEGV	120	10	2803
PSM	LAGAKGVI	219	8	2804
PSM	LAGAKGVIL	219	9	2805
PSM	LAGAKGVILY	219	10	2806
PSM	LAGGFFLL	28	8	2807
PSM	LAGGFFLLGF	28	10	2808
PSM	LAGGFFLLGFL	28	11	2809
PSM	LAGTEQNF	83	8	2810
PSM	LAGTEQNFQL	83	10	2811
PSM	LAGTEQNFQLA	83	11	2812
PSM	LAHYDVLL	110	8	2813
PSM	LAHYDVLLSY	110	10	2814
PAP	LAKELKFV	31	8	2815
PAP	LAKELKFVTL	31	10	2816
PAP	LAKELKFVTLV	31	11	2817
PSM	LAKQIQSQW	92	9	2818
PSM	LANSIVLPF	587	9	2819
PAP	LARAASLSL	8	9	2820
PAP	LARAASLSLGF	8	11	2821
PAP	LSEDQLLY	148	8	2822
PAP	LSEDQLLYL	148	9	2823
PAP	LSEDQLLYLPF	148	11	2824
PAP	LSELSLLSL	238	9	2825
PAP	LSELSLLSLY	238	10	2826
PSA	LSEPAELTDA	122	10	2827
PSA	LSEPAELTDAV	122	11	2828
Kallikrein	LSEPAKITDV	126	10	2829
Kallikrein	LSEPAKITDVV	126	11	2830
PAP	LSGLHGQDL	194	9	2831
PAP	LSGLHGQDLF	194	10	2832
PAP	LSLGFLFL	14	8	2833
PAP	LSLGFLFLL	14	9	2834
PAP	LSLGFLFLLF	14	10	2835
PAP	LSLGFLFLLFF	14	11	2836
PAP	LSLLSLYGI	241	9	2837
Kallikrein	LSNDMCARA	179	9	2838
Kallikrein	LSNDMCARAY	179	10	2839
PSA	LSRIVGGW	18	8	2840
Kallikrein	LSVGCTGA	10	8	2841
Kallikrein	LSVGCTGAV	10	9	2842
Kallikrein	LSVGCTGAVPL	10	11	2843
PSA	LSVTWIGA	6	8	2844
PSA	LSVTWIGAA	6	9	2845
PSA	LSVTWIGAAPL	6	11	2846

Table XLII

Prostate B58 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	LSYPNKTHPNY	117	11	2847
PSA	LTDAVKVM	128	8	2848
PSA	LTDAVKVMDL	128	10	2849
PAP	LTELYFEKGEY	315	11	2850
PSA	LTLSVTWI	4	8	2851
PSA	LTLSVTWIGA	4	10	2852
PSA	LTLSVTWIGAA	4	11	2853
PSM	LTPGYPANEY	268	10	2854
PSM	LTPGYPANEYA	268	11	2855
PSA	LTPKKLQCV	162	9	2856
PSA	LTPKKLQCVDL	162	11	2857
PAP	LTQLGMEQHY	70	10	2858
PSM	LTVAQVRGGM	574	10	2859
PSM	LTVAQVRGGMV	574	11	2860
PAP	MALDVYNGL	298	9	2861
PAP	MALDVYNGLL	298	10	2862
PAP	MSAMTNLA	114	8	2863
PAP	MSAMTNLAA	114	9	2864
PAP	MSAMTNLAAL	114	10	2865
PAP	MSAMTNLAALF	114	11	2866
Kallikrein	MSLLKHQSL	103	9	2867
PSA	MSLLKNRF	99	8	2868
PSA	MSLLKNRFL	99	9	2869
PAP	MTKLRELSEL	232	10	2870
PAP	MTNLAALF	117	8	2871
PSM	NADSSIEGNY	451	10	2872
PSM	NAQLAGAKGV	216	10	2873
PSM	NAQLAGAKGVI	216	11	2874
Kallikrein	NSQVWLGRHNL	70	11	2875
PSM	NSRLLQERGV	438	10	2876
PSM	NSRLLQERGVA	438	11	2877
PSM	PADYFAPGV	231	9	2878
PSA	PAELTDAV	125	8	2879
PSA	PAELTDAVKV	125	10	2880
PSA	PAELTDAVKVM	125	11	2881
Kallikrein	PAKITDVV	129	8	2882
Kallikrein	PAKITDVVKV	129	10	2883
Kallikrein	PAKITDVVKVL	129	11	2884
Kallikrein	PALGTTCY	146	8	2885
PSA	PALGTTCY	142	8	2886
Kallikrein	PALGTTCYA	146	9	2887
PSA	PALGTTCYA	142	9	2888
PSM	PANEYAYRRGI	273	11	2889
Kallikrein	PAVYTKVV	240	8	2890

Table XIII
Prostate B58 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
Kallikrein	PAVYTKVVHY	240	10	2891
PAP	PSCPLERF	349	8	2892
PAP	PSCPLERFA	349	9	2893
PAP	PSCPLERFAEL	349	11	2894
PSM	PSIPVHPI	290	8	2895
PSM	PSIPVHPIGY	290	10	2896
PSM	PSIPVHPIGYY	290	11	2897
PSM	PSKAWGEV	721	8	2898
PSA	PSLYTKVV	236	8	2899
PSA	PSLYTKVVHY	236	10	2900
PSM	PSPEFSGM	502	8	2901
PSM	PSPEFSGMPRI	502	11	2902
PSM	PSSHNKYA	694	8	2903
PAP	PSWATEDTM	224	9	2904
PAP	PSYKKLIM	278	8	2905
PAP	PSYKKLIMY	278	9	2906
PAP	PSYKKLIMYSA	278	11	2907
PAP	PTDPIKESSW	54	10	2908
PSM	QAAAETLSEV	740	10	2909
PSM	QAAAETLSEVA	740	11	2910
PSM	QSGAAVVHEI	389	10	2911
PSM	QSGAAVVHEIV	389	11	2912
PSM	QSQWKEFGL	97	9	2913
Kallikrein	QSRIVGGW	22	8	2914
PAP	RAAPLLLA	2	8	2915
PAP	RAAPLLLARA	2	10	2916
PAP	RAAPLLLARAA	2	11	2917
PAP	RAASLSLGF	10	9	2918
PAP	RAASLSLGFL	10	10	2919
PAP	RAASLSLGFLF	10	11	2920
PSM	RAFIDPLGL	673	9	2921
PSM	RARYTKNW	534	8	2922
PAP	RATQIPSY	273	8	2923
PAP	RATQIPSYKKL	273	11	2924
PSA	RAVCGGVL	43	8	2925
PSA	RAVCGGVLV	43	9	2926
Kallikrein	RAYSEKVTEF	186	10	2927
Kallikrein	RAYSEKVTEFM	186	11	2928
PSM	RSFGTLKKEGW	400	11	2929
Kallikrein	RSLQCVSL	169	8	2930
Kallikrein	RSLQCVSLHL	169	10	2931
Kallikrein	RSLQCVSLHLL	169	11	2932
PAP	RSTDVDRTL	105	9	2933
PAP	RSTDVDRTLM	105	10	2934

Table XIII

Prostate B58 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PAP	RSVLAKEL	28	8	2935
PAP	RSVLAKELKF	28	10	2936
PAP	RSVLAKELKFV	28	11	2937
PSM	RTEDFFKL	181	8	2938
PSM	RTILFASW	414	8	2939
PSM	RTILFASWDA	414	10	2940
PAP	RTLMSAMTNL	111	10	2941
PAP	RTLMSAMTNLA	111	11	2942
PSM	SAFSPQGM	162	8	2943
PAP	SAHDTTVSGL	287	10	2944
PAP	SAMTNLAA	115	8	2945
PAP	SAMTNLAAL	115	9	2946
PAP	SAMTNLAALF	115	10	2947
PSM	SAPPDSSW	312	8	2948
PSM	SAVATARRPRW	10	11	2949
PSM	SAVKNFTEI	634	9	2950
PSM	SAVKNFTEIA	634	10	2951
Kallikrein	SSHDLMLL	117	8	2952
PSA	SSHDLMLL	113	8	2953
Kallikrein	SSHDLMLLRL	117	10	2954
PSA	SSHDLMLLRL	113	10	2955
PSM	SSHNKYAGESF	695	11	2956
PSM	SSIEGNYTL	454	9	2957
PSM	SSIEGNYTLRV	454	11	2958
PSM	SSNEATNI	45	8	2959
PAP	SSWPQGFGQL	61	10	2960
PSM	SSWRGSLKV	317	9	2961
PSM	SSWRGSLKVPY	317	11	2962
PSA	STCSGDSGGPL	203	11	2963
PAP	STDVDRTL	106	8	2964
PAP	STDVDRTLM	106	9	2965
PAP	STDVDRTLMSA	106	11	2966
PSM	STEWAEENSRL	431	11	2967
PSM	STNEVTRI	348	8	2968
PSM	STNEVTRIY	348	9	2969
PSM	STNEVTRIYNV	348	11	2970
PSM	STQKVKMHI	338	9	2971
PSA	TAAHCIRNKSV	58	11	2972
PSM	TARRPRWL	14	8	2973
PSM	TARRPRWLCA	14	10	2974
PSM	TSLFEPPPPGY	141	11	2975
Kallikrein	TSWGPEPCA	227	9	2976
Kallikrein	TSWGPEPCAL	227	10	2977
PSA	TSWGSEPCA	223	9	2978

Table XII

Prostate B58 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSA	TSWGSEPCAL	223	10	2979
Kallikrein	TTCYASGW	150	8	2980
PSA	TTCYASGW	146	8	2981
Kallikrein	TTCYASGWGSI	150	11	2982
PSA	TTCYASGWGSI	146	11	2983
PAP	TTVSGLQM	291	8	2984
PAP	TTVSGLQMA	291	9	2985
PAP	TTVSGLQMAL	291	10	2986
PSM	VAAFTVQA	734	8	2987
PSM	VAAFTVQAA	734	9	2988
PSM	VAAFTVQAAA	734	10	2989
PSM	VAQVRGGM	576	8	2990
PSM	VAQVRGGMV	576	9	2991
PSM	VAQVRGGMVF	576	10	2992
PSA	VASRGRAV	38	8	2993
PSM	VATARRPRW	12	9	2994
PSM	VATARRPRWL	12	10	2995
Kallikrein	VAVYSHGW	40	8	2996
Kallikrein	VAVYSHGWA	40	9	2997
PSM	VAYINADSSI	447	10	2998
PSM	VSDIVPPF	154	8	2999
PSM	VSDIVPPFSA	154	10	3000
PSM	VSDIVPPFSAF	154	11	3001
PSM	VSFDSLFSA	627	9	3002
PSM	VSFDSLFSAV	627	10	3003
PAP	VSGLQMAL	293	8	3004
PAP	VSGLQMALDV	293	10	3005
PAP	VSGLQMALDVY	293	11	3006
Kallikrein	VSHSFPHPL	92	9	3007
PSA	VSHSFPHPL	88	9	3008
Kallikrein	VSHSFPHPLY	92	10	3009
PSA	VSHSFPHPLY	88	10	3010
PAP	VSIWNPIL	129	8	3011
PAP	VSIWNPILL	129	9	3012
PAP	VSIWNPILLW	129	10	3013
Kallikrein	VSLHLLSNDM	174	10	3014
Kallikrein	VTEFMLCA	192	8	3015
Kallikrein	VTEFMLCAGL	192	10	3016
Kallikrein	VTEFMLCAGLW	192	11	3017
PSA	VTKFMLCA	188	8	3018
PSA	VTKFMLCAGRW	188	11	3019
PSM	VTRIYNVI	352	8	3020
PSM	VTRIYNVIGTL	352	11	3021
PSA	VTWIGAAPL	8	9	3022

Table XIII

Prostate B58 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSA	VTWIGAAPLI	8	10	3023
PSA	VTWIGAAPLIL	8	11	3024
PSM	WAEENSRL	434	8	3025
PSM	WAEENSRLL	434	9	3026
Kallikrein	WAHCGGVL	47	8	3027
Kallikrein	WAHCGGVLV	47	9	3028
PAP	WATEDTMTKL	226	10	3029
PAP	WSKVYDPL	206	8	3030
PAP	WSKVYDPLY	206	9	3031
PSM	WTKKSPSPEF	497	10	3032
PSM	YADKIYSI	607	8	3033
PSM	YADKIYSISM	607	10	3034
PSM	YAGESFPGI	700	9	3035
PSM	YAGESFPGIY	700	10	3036
PSM	YAPSSHNKY	692	9	3037
PSM	YAPSSHNKYA	692	10	3038
PSM	YARTEDFF	179	8	3039
PSM	YARTEDFFKL	179	10	3040
PAP	YASCHLTEL	310	9	3041
PAP	YASCHLTELY	310	10	3042
PAP	YASCHLTELYF	310	11	3043
Kallikrein	YASGWGSI	153	8	3044
PSA	YASGWGSI	149	8	3045
PSM	YAVVLRKY	600	8	3046
PSM	YAVVLRKYA	600	9	3047
PSM	YAYRRGIA	277	8	3048
PSM	YAYRRGIAEA	277	10	3049
PSM	YAYRRGIAEAV	277	11	3050
PAP	YSAHDTTV	286	8	3051
PAP	YSAHDTTVSGL	286	11	3052
PSM	YSDPADYF	228	8	3053
PSM	YSDPADYFA	228	9	3054
Kallikrein	YSEKVTEF	188	8	3055
Kallikrein	YSEKVTEFM	188	9	3056
Kallikrein	YSEKVTEFML	188	10	3057
Kallikrein	YSHGWAHCGGV	43	11	3058
PSM	YSISMKHPQEM	612	11	3059
PSM	YSLVHNLTKEL	471	11	3060
PSM	YSVSFDSL	625	8	3061
PSM	YSVSFDSLF	625	9	3062
PSM	YSVSFDSLFSA	625	11	3063
PSM	YTKNWETNKF	537	10	3064
Kallikrein	YTKVVHYRKW	243	10	3065
PSA	YTKVVHYRKW	239	10	3066

Table XIII

Prostate B58 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
Kallikrein	YTKVVHYRKWI	243	11	3067
PSA	YTKVVHYRKWI	239	11	3068
PSM	YTLRVDCTPL	460	10	3069
PSM	YTLRVDCTPLM	460	11	3070

Table XIV
Prostate-B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PAP	ALDVYNGL	299	8	3071
PAP	ALDVYNGLL	299	9	3072
PSM	ALFDIESKV	711	9	3073
PAP	ALFPPEGV	122	8	3074
PAP	ALFPPEGVSI	122	10	3075
PAP	ALFPPEGVSIW	122	11	3076
Kallikrein	ALGTTCYA	147	8	3077
PSA	ALGTTCYA	143	8	3078
Kallikrein	ALGTTCYASGW	147	11	3079
PSA	ALGTTCYASGW	143	11	3080
Kallikrein	ALPEKPAV	235	8	3081
Kallikrein	ALPEKPAVY	235	9	3082
PSA	ALPERPSL	231	8	3083
PSA	ALPERPSLY	231	9	3084
Kallikrein	ALSVGCTGA	9	9	3085
Kallikrein	ALSVGCTGAV	9	10	3086
PSM	ALVLAGGF	25	8	3087
PSM	ALVLAGGFF	25	9	3088
PSM	ALVLAGGFFL	25	10	3089
PSM	ALVLAGGFFLL	25	11	3090
PAP	AMTNLAAL	116	8	3091
PAP	AMTNLAALF	116	9	3092
PSM	APGVKSYPDGW	236	11	3093
PSA	APLILSRI	14	8	3094
PSA	APLILSRIV	14	9	3095
PAP	APLLLARA	4	8	3096
PAP	APLLLARAA	4	9	3097
PAP	APLLLARAASL	4	11	3098
PSM	APPDSSWRGSL	313	11	3099
PSM	APSSHNKY	693	8	3100
PSM	APSSHNKYA	693	9	3101
PSM	AQKLLEKM	302	8	3102
PSM	AQLAGAKGV	217	9	3103
PSM	AQLAGAKGVI	217	10	3104
PSM	AQLAGAKGVIL	217	11	3105
PSA	AQVHPQKV	181	8	3106
PSA	AQVHPQKVTKF	181	11	3107
PSM	AQVRGGMV	577	8	3108
PSM	AQVRGGMVF	577	9	3109
PSM	AQVRGGMVFEL	577	11	3110
PSM	AVATARRPRW	11	10	3111
PSM	AVATARRPRWL	11	11	3112
PSA	AVCGGVLV	44	8	3113
PSM	AVEPDRYV	365	8	3114

Table XIV

Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	AVEPDRYVI	365	9	3115
PSM	AVEPDRYVIL	365	10	3116
PSM	AVGLPSIPV	286	9	3117
PSM	AVKNFTEI	635	8	3118
PSM	AVKNFTEIA	635	9	3119
Kallikrein	AVPLIQSRI	17	9	3120
Kallikrein	AVPLIQSRIV	17	10	3121
PSM	AVVHEIVRSF	393	10	3122
PSM	AVVLRKYA	601	8	3123
PSM	AVVLRKYADKI	601	11	3124
Kallikrein	AVYSHGWA	41	8	3125
Kallikrein	AVYTKVVHY	241	9	3126
PSA	CIRNKSVI	62	8	3127
PSA	CIRNKSVIL	62	9	3128
PSA	CIRNKSVILL	62	10	3129
Kallikrein	CLKKNSQV	66	8	3130
Kallikrein	CLKKNSQVW	66	9	3131
Kallikrein	CLKKNSQVWL	66	10	3132
PAP	CPLERFAEL	351	9	3133
PAP	CPLERFAELV	351	10	3134
PSA	CVDLHVISNDV	169	11	3135
Kallikrein	CVSLHLLSNDM	173	11	3136
PSM	DIESKVDPSKA	714	11	3137
PSM	DIVPPFSA	156	11	3138
PSM	DIVPPFSAF	156	8	3139
PAP	DLFGIWSKV	201	9	3140
PAP	DLFGIWSKVY	201	9	3141
PSA	DLHVISNDV	171	10	3142
PSA	DLHVISNDVCA	171	9	3143
Kallikrein	DLMLLRLSEPA	120	11	3144
PSA	DLMLLRLSEPA	116	11	3145
PSA	DLPTQEPA	136	11	3146
PSA	DLPTQEPAL	136	8	3147
PSA	DLVLSIAL	3	9	3148
Kallikrein	DLVLSIALSV	3	8	3149
Kallikrein	DLVYVNYA	173	10	3150
PSM	DMCARAYSEKV	182	8	3151
Kallikrein	DMKINCSGKI	191	11	3152
PSM	DMKINCSGKIV	191	10	3153
PSM	DMSLLKNRF	98	11	3154
PSA	DMSLLKNRFL	98	9	3155
PSA	DPADYFAPGV	230	10	3156
PSM	DPIKESSW	56	10	3157
PAP	DPLGLPDRPF	677	8	3158
PSM			10	

Table XIV

Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	DPLGLPDRPFY	677	11	3159
PSM	DPLTPGYPA	266	9	3160
PAP	DPLYCESV	211	8	3161
PAP	DPLYCESVHNF	211	11	3162
PSM	DPMFKYHL	567	8	3163
PSM	DPMFKYHLTV	567	10	3164
PSM	DPMFKYHLTVA	567	11	3165
PSM	DPQSGAAV	387	8	3166
PSM	DPQSGAAVV	387	9	3167
PSM	DPSKAWGEV	720	9	3168
PAP	DQLLYLPF	151	8	3169
PSM	DQLMFLERA	666	9	3170
PSM	DQLMFLERAF	666	10	3171
PSM	DQLMFLERAFI	666	11	3172
PSA	DVCAQVHPQKV	178	11	3173
PAP	DVDRTLMSA	108	9	3174
PAP	DVDRTLMSAM	108	10	3175
Kallikrein	DVVKVLGL	134	8	3176
PAP	DVYNGLLPPY	301	10	3177
PAP	DVYNGLLPPYA	301	11	3178
PSM	EIASKFSERL	641	10	3179
PSM	EIFNTSLF	137	8	3180
PAP	EILNHMKRA	266	9	3181
PSM	EIVRSFGTL	397	9	3182
PSM	ELAHYDVL	109	8	3183
PSM	ELAHYDVLL	109	9	3184
PSM	ELAHYDVLLSY	109	11	3185
PSM	ELANSIVL	586	8	3186
PSM	ELANSIVLPF	586	10	3187
PAP	ELGEYIRKRY	80	10	3188
PSM	ELKAENIKKF	64	10	3189
PSM	ELKAENIKKFL	64	11	3190
PAP	ELKFVTLV	34	8	3191
PAP	ELKFVTLVF	34	9	3192
PSM	ELKSPDEGF	480	9	3193
PAP	ELSELSLL	237	8	3194
PAP	ELSELSLLSL	237	10	3195
PAP	ELSELSLLSLY	237	11	3196
PAP	ELSLLSLY	240	8	3197
PAP	ELSLLSLYGI	240	10	3198
PSA	ELTDAVKV	127	8	3199
PSA	ELTDAVKVM	127	9	3200
PSA	ELTDAVKVMDL	127	11	3201
PSM	ELVEKFYDPM	560	10	3202

Table XIV
Prostate B62 Supermatrix with Blosum Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	ELVEKFYDPMF	560	11	3203
PAP	ELVGPVIPQDW	358	11	3204
PAP	ELYFEKGEY	317	9	3205
PAP	ELYFEKGEYF	317	10	3206
PAP	ELYFEKGEYFV	317	11	3207
PSM	EMKTYSVSF	621	9	3208
PSA	EPAELTDA	124	8	3209
PSA	EPAELTDAV	124	9	3210
PSA	EPAELTDAVKV	124	11	3211
Kallikrein	EPAKITDV	128	8	3212
Kallikrein	EPAKITDVV	128	9	3213
Kallikrein	EPAKITDVVKV	128	11	3214
Kallikrein	EPALGTTCY	145	9	3215
PSA	EPALGTTCY	141	9	3216
Kallikrein	EPALGTTCYA	145	10	3217
PSA	EPALGTTCYA	141	10	3218
Kallikrein	EPCALPEKPA	232	10	3219
Kallikrein	EPCALPEKPAV	232	11	3220
PSA	EPCALPERPSL	228	11	3221
PSM	EPDRYVIL	367	8	3222
Kallikrein	EPEDTGQRV	82	9	3223
Kallikrein	EPEDTGQRVPV	82	11	3224
Kallikrein	EPEEFLRPRSL	161	11	3225
PSA	EPEEFLTPKKL	157	11	3226
PSM	EPPPPGYENV	145	10	3227
PAP	EQHYELGEY	76	9	3228
PAP	EQHYELGEYI	76	10	3229
PSM	EQNFQLAKQI	87	10	3230
PAP	EQVYIRSTDV	100	10	3231
PSM	EVFFQRLGI	522	9	3232
PSM	EVFFQRLGIA	522	10	3233
PSM	EVKRQIYV	727	8	3234
PSM	EVKRQIYVA	727	9	3235
PSM	EVKRQIYVAA	727	10	3236
PSM	EVKRQIYVAAF	727	11	3237
PSM	EVTRIYNV	351	8	3238
PSM	EVTRIYNVI	351	9	3239
PAP	FIATLGKL	187	8	3240
PAP	FIATLGKLSGL	187	11	3241
PSM	FIKSSNEA	42	8	3242
PSM	FIKSSNEATNI	42	11	3243
PSM	FLDELKAENI	61	10	3244
PSM	FLERAFIDPL	670	10	3245
PAP	FLFLLFFW	18	8	3246

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Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PAP	FLFLLFFWL	18	9	3247
PAP	FLLFFWLDRSV	20	11	3248
PSM	FLLGFLFGW	33	9	3249
PSM	FLLGFLFGWF	33	10	3250
PSM	FLLGFLFGWFI	33	11	3251
PAP	FLNESYKHEQV	92	11	3252
Kallikrein	FLRPRSLQCV	165	10	3253
PSA	FLTLSVTW	3	8	3254
PSA	FLTLSVTWI	3	9	3255
PSA	FLTLSVTWIGA	3	11	3256
PSA	FLTPKKLQCV	161	10	3257
PSM	FLYNFTQI	73	8	3258
PSM	FLYNFTQIPHL	73	11	3259
Kallikrein	FMLCAGLW	195	8	3260
PSA	FMLCAGRW	191	8	3261
PSM	FPGIYDAL	705	8	3262
PSM	FPGIYDALF	705	9	3263
PSM	FPGIYDALFDI	705	11	3264
PSA	FPHPLYDM	92	8	3265
PSA	FPHPLYDMSL	92	10	3266
PSA	FPHPLYDMSLL	92	11	3267
Kallikrein	FPHPLYNM	96	8	3268
Kallikrein	FPHPLYNMSL	96	10	3269
Kallikrein	FPHPLYNMSLL	96	11	3270
PAP	FPPEGVSI	124	8	3271
PAP	FPPEGVSIW	124	9	3272
PAP	FPTDPIKESSW	53	11	3273
PAP	FQELESETL	164	9	3274
PAP	FQKRLHPY	177	8	3275
PAP	FQKRLHPYKDF	177	11	3276
PSM	FQLAKQIQSQW	90	11	3277
PSM	FQRLGIASGRA	525	11	3278
PSA	FQVSHSFPHPL	86	11	3279
PSM	GIAEAVGL	282	8	3280
PSM	GIAEAVGLPSI	282	11	3281
PSM	GIASGRARY	529	9	3282
PSM	GIDPQSGA	385	8	3283
PSM	GIDPQSGAA	385	9	3284
PSM	GIDPQSGAAV	385	10	3285
PSM	GIDPQSGAAVV	385	11	3286
PAP	GIHKQKEKSRL	248	11	3287
Kallikrein	GITSWGPEPCA	225	11	3288
PSA	GITSWGSEPCA	221	11	3289
PAP	GIWSKVYDPL	204	10	3290

Table XIV

Prostate B62 Supermotifs with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PAP	GIWSKVYDPLY	204	11	3291
PSM	GIYDALFDI	707	9	3292
PSM	GLDSVELA	104	8	3293
PSM	GLDSVELAHY	104	10	3294
PAP	GLHGQDLF	196	8	3295
PAP	GLHGQDLFGI	196	10	3296
PAP	GLHGQDLFGIW	196	11	3297
PSM	GLLGSTEW	427	8	3298
PSM	GLLGSTEWA	427	9	3299
PAP	GLLPPYASCHL	305	11	3300
PSM	GLPDRPFY	680	8	3301
PSM	GLPDRPFYRHV	680	11	3302
PSM	GLPSIPVHPI	288	10	3303
Kallikrein	GLPTQEPA	140	8	3304
Kallikrein	GLPTQEPAL	140	9	3305
PAP	GLQMALDV	295	8	3306
PAP	GLQMALDVY	295	9	3307
PAP	GMEQHYEL	74	8	3308
PAP	GMEQHYELGEY	74	11	3309
PSM	GMPEGDLV	168	8	3310
PSM	GMPEGDLVY	168	9	3311
PSM	GMPEGDLVYV	168	10	3312
PSM	GMPRISKL	508	8	3313
PSM	GMVFELANSI	582	10	3314
PSM	GMVFELANSIV	582	11	3315
PSM	GPGFTGNF	330	8	3316
Kallikrein	GPLVCNGV	215	8	3317
PSA	GPLVCNGV	211	8	3318
Kallikrein	GPLVCNGVL	215	9	3319
PSA	GPLVCNGVL	211	9	3320
PAP	GPVIPQDW	361	8	3321
PAP	GQDLFGIW	199	8	3322
PAP	GQDLFGIWSKV	199	11	3323
PAP	GQLTQLGM	68	8	3324
Kallikrein	GQRVPVSHSF	87	10	3325
PSA	GQVFQVSHSF	83	10	3326
PSM	GVAYINADSSI	446	11	3327
PSM	GVILYSDPA	224	9	3328
PSM	GVILYSDPADY	224	11	3329
PSM	GVKSYPDGW	238	9	3330
PSM	GVKSYPDGWNL	238	11	3331
Kallikrein	GVLQGITSW	221	9	3332
PSA	GVLQGITSW	217	9	3333
Kallikrein	GVLVHPQW	52	8	3334

Table XIV
Prostate B62 Supermotif MHC Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSA	GVLVHPQW	48	8	3335
Kallikrein	GVLVHPQWV	52	9	3336
PSA	GVLVHPQWV	48	9	3337
Kallikrein	GVLVHPQWVL	52	10	3338
PSA	GVLVHPQWVL	48	10	3339
PAP	GVLVNEIL	261	8	3340
PAP	GVLVNEILNHM	261	11	3341
PSM	GVQRGNIL	252	8	3342
PSM	GVQRGNILNL	252	10	3343
PAP	GVSIWNPI	128	8	3344
PAP	GVSIWNPIL	128	9	3345
PAP	GVSIWNPILL	128	10	3346
PAP	GVSIWNPILLW	128	11	3347
PSM	HIHSTNEV	345	8	3348
PSM	HIHSTNEVTRI	345	11	3349
PSM	HLAGTEQNF	82	9	3350
PSM	HLAGTEQNFQL	82	11	3351
Kallikrein	HLLSNDMCA	177	9	3352
Kallikrein	HLLSNDMCARA	177	11	3353
PSM	HLTVAQVRGGM	573	11	3354
PAP	HMKRATQI	270	8	3355
PAP	HMKRATQIPSY	270	11	3356
PSA	HPEDTGQV	78	8	3357
PSA	HPEDTGQVF	78	9	3358
PSA	HPEDTGQVFQV	78	11	3359
PSM	HPIGYYDA	295	8	3360
PSM	HPIGYYDAQKL	295	11	3361
PSA	HPLYDMSL	94	8	3362
PSA	HPLYDMSLL	94	9	3363
Kallikrein	HPLYNMSL	98	8	3364
Kallikrein	HPLYNMSLL	98	9	3365
PSM	HPNYISII	124	8	3366
PSM	HPQEMKTY	618	8	3367
PSM	HPQEMKTYSV	618	10	3368
PSA	HPQKVTKF	184	8	3369
PSA	HPQKVTKFM	184	9	3370
PSA	HPQKVTKFML	184	10	3371
Kallikrein	HPQWVLTA	56	8	3372
PSA	HPQWVLTA	52	8	3373
Kallikrein	HPQWVLTAA	56	9	3374
PSA	HPQWVLTAA	52	9	3375
PAP	HPYKDFIA	182	8	3376
PAP	HPYKDFIATL	182	10	3377
PSA	HVISNDVCA	173	9	3378

Table XIV

Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSA	HVISNDVCAQV	173	11	3379
PSM	IINEDGNEI	130	9	3380
PSM	IINEDGNEIF	130	10	3381
PSM	ILFASWDA	416	8	3382
PSM	ILFASWDAEEF	416	11	3383
PSM	ILGGHRDSW	373	9	3384
PSM	ILGGHRDSWV	373	10	3385
PSM	ILGGHRDSWVF	373	11	3386
PSA	ILLGRHSL	69	8	3387
PSA	ILLGRHSLF	69	9	3388
PAP	ILLWQPIPV	135	9	3389
PAP	ILNIMKRA	267	8	3390
PAP	ILNIMKRATQI	267	11	3391
PSM	ILNLNGAGDPL	258	11	3392
PSA	ILSRIVGGW	17	9	3393
PSM	ILYSDPADY	226	9	3394
PSM	ILYSDPADYF	226	10	3395
PSM	ILYSDPADYFA	226	11	3396
PAP	IMYSAHDTTV	284	10	3397
PSM	IPHLAGTEQNF	80	11	3398
PAP	IPQDWSTECM	364	10	3399
PAP	IPSYKKLI	277	8	3400
PAP	IPSYKKLIM	277	9	3401
PAP	IPSYKKLIMY	277	10	3402
PSM	IPVHIPIGY	292	8	3403
PSM	IPVHPIGYY	292	9	3404
PSM	IPVHPIGYYDA	292	11	3405
PAP	IPVHTVPL	141	8	3406
PSM	IQSQWKEF	96	8	3407
PSM	IQSQWKEFGL	96	10	3408
Kallikrein	IQSRIVGGW	21	9	3409
PSM	IVIARYGKV	200	9	3410
PSM	IVIARYGKVF	200	10	3411
PSM	IVLPFDCRDY	591	10	3412
PSM	IVLPFDCRDYA	591	11	3413
PSM	IVLRMMNDQL	659	10	3414
PSM	IVLRMMNDQLM	659	11	3415
PSM	IVPPFSAF	157	8	3416
PSM	IVRSFGTL	398	8	3417
PSM	KINCSGKI	193	8	3418
PSM	KINCSGKIV	193	9	3419
PSM	KINCSGKIVI	193	10	3420
PSM	KINCSGKIVIA	193	11	3421
Kallikrein	KITDVVKV	131	8	3422

Table XIV

Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
Kallikrein	KITDVVKVL	131	9	3423
Kallikrein	KITDVVKVLGL	131	11	3424
PSM	KIVIARYGKV	199	10	3425
PSM	KIVIARYGKVF	199	11	3426
PSM	KLERDMKI	187	8	3427
PSM	KLGSGNDF	514	8	3428
PSM	KLGSGNDFEV	514	10	3429
PSM	KLGSGNDFEVF	514	11	3430
PSM	KLLEKMGGSA	304	10	3431
PSA	KLQCVDLHV	166	9	3432
PSA	KLQCVDLHVI	166	10	3433
PAP	KLRELSEL	234	8	3434
PAP	KLRELSELSL	234	10	3435
PAP	KLRELSELSLL	234	11	3436
PAP	KLSGLHGQDL	193	10	3437
PAP	KLSGLHGQDLF	193	11	3438
PSM	KMHHHSTNEV	343	10	3439
Kallikrein	KPAVYTKV	239	8	3440
Kallikrein	KPAVYTKVV	239	9	3441
Kallikrein	KPAVYTKVVHY	239	11	3442
PSM	KQIQSQWKEF	94	10	3443
PAP	KQKEKSRL	251	8	3444
PSM	KVDPSKAW	718	8	3445
PSM	KVDPSKAWGEV	718	11	3446
PSM	KVFRGNKV	207	8	3447
PSM	KVFRGNKVKNA	207	11	3448
PSM	KVKNAQLA	213	8	3449
PSM	KVKNAQLAGA	213	10	3450
Kallikrein	KVLGLPTQEPA	137	11	3451
PSA	KVMDLPTQEPA	133	11	3452
PSM	KVPYNVGPGF	324	10	3453
Kallikrein	KVTEFMLCA	191	9	3454
Kallikrein	KVTEFMLCAGL	191	11	3455
PSA	KVTKFMLCA	187	9	3456
Kallikrein	KVVHYRKW	245	8	3457
PSA	KVVHYRKW	241	8	3458
Kallikrein	KVVHYRKWI	245	9	3459
PSA	KVVHYRKWI	241	9	3460
PAP	KVYDPLYCESV	208	11	3461
PSA	LILSRIVGGW	16	10	3462
PAP	LIMYSAHDTTV	283	11	3463
Kallikrein	LIQSRIVGGW	20	10	3464
PAP	LLARAASL	7	8	3465
PAP	LLARAASLSL	7	10	3466

Table XIV
Prostate 362 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	LLEKMGGSA	305	9	3467
PAP	LLFFWLDRSV	21	10	3468
PAP	LLFFWLDRSVL	21	11	3469
PSM	LLGFLFGW	34	8	3470
PSM	LLGFLFGWF	34	9	3471
PSM	LLGFLFGWFI	34	10	3472
PSA	LLGRHSLF	70	8	3473
PSM	LLGSTEWA	428	8	3474
PSM	LLHETDSA	4	8	3475
PSM	LLHETDSAV	4	9	3476
PSM	LLHETDSAVA	4	10	3477
PAP	LLLARAASL	6	9	3478
PAP	LLLARAASLSL	6	11	3479
PAP	LLPPYASCHL	306	10	3480
PSM	LLQERGVA	441	8	3481
PSM	LLQERGVAY	441	9	3482
PSM	LLQERGVAYI	441	10	3483
Kallikrein	LLRLSEPA	123	8	3484
PSA	LLRLSEPA	119	8	3485
PSA	LLRLSEPAEL	119	10	3486
Kallikrein	LLRLSEPAKI	123	10	3487
Kallikrein	LLSNDMCA	178	8	3488
Kallikrein	LLSNDMCARA	178	10	3489
Kallikrein	LLSNDMCARAY	178	11	3490
PAP	LLWQPIPV	136	8	3491
PAP	LLWQPIPVHTV	136	11	3492
PSM	LMFLERAF	668	8	3493
PSM	LMFLERAFI	668	9	3494
Kallikrein	LMLLRLSEPA	121	10	3495
PSA	LMLLRLSEPA	117	10	3496
PAP	LMSAMTNL	113	8	3497
PAP	LMSAMTNLA	113	9	3498
PAP	LMSAMTNLAA	113	10	3499
PAP	LMSAMTNLAAL	113	11	3500
PSM	LMYSLVHNL	469	9	3501
PSM	LPDRPFYRHV	681	10	3502
PSM	LPDRPFYRHVI	681	11	3503
Kallikrein	LPEKPAVY	236	8	3504
Kallikrein	LPEKPAVYTKV	236	11	3505
PSA	LPERPSLY	232	8	3506
PSA	LPERPSLYTKV	232	11	3507
PSM	LPFDCRDY	593	8	3508
PSM	LPFDCRDYA	593	9	3509
PSM	LPFDCRDYAV	593	10	3510

Table XIV

Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	LPFDCRDYAVV	593	11	3511
PAP	LPFRNCPRF	156	9	3512
PAP	LPGCSPSCPL	344	10	3513
PSM	LPGGGVQRGNI	248	11	3514
PAP	LPPYASCHL	307	9	3515
PSM	LPSIPVHPI	289	9	3516
PSM	LPSIPVHPIGY	289	11	3517
PAP	LPSWATEDTM	223	10	3518
Kallikrein	LPTQEPAL	141	8	3519
PSA	LPTQEPAL	137	8	3520
PSA	LQCVDLHV	167	8	3521
PSA	LQCVDLHVI	167	9	3522
Kallikrein	LQCVSLHL	171	8	3523
Kallikrein	LQCVSLHLL	171	9	3524
PSM	LQDFDKSNPI	650	10	3525
PSM	LQDFDKSNPIV	650	11	3526
PSM	LQERGVAY	442	8	3527
PSM	LQERGVAYI	442	9	3528
PSM	LQERGVAYINA	442	11	3529
PAP	LQGGVLVNEI	258	10	3530
PAP	LQGGVLVNEIL	258	11	3531
PAP	LQMALDVY	296	8	3532
PAP	LQMALDVYNGL	296	11	3533
PSA	LVASRGRA	37	8	3534
PSA	LVASRGRAV	37	9	3535
Kallikrein	LVCNGVLQGI	217	10	3536
PSA	LVCNGVLQGI	213	10	3537
PSM	LVEKFYDPM	561	9	3538
PSM	LVEKFYDPMF	561	10	3539
PAP	LVFRHGDRSPI	40	11	3540
PAP	LVGPVIPQDW	359	10	3541
PSM	LVHNLTKEL	473	9	3542
Kallikrein	LVHPQWVL	54	8	3543
PSA	LVHPQWVL	50	8	3544
Kallikrein	LVHPQWVLTA	54	10	3545
PSA	LVHPQWVLTA	50	10	3546
Kallikrein	LVHPQWVLTAA	54	11	3547
PSA	LVHPQWVLTAA	50	11	3548
PSM	LVLAGGFF	26	8	3549
PSM	LVLAGGFFL	26	9	3550
PSM	LVLAGGFFLL	26	10	3551
Kallikrein	LVLSIALSV	4	9	3552
PAP	LVNEILNHM	263	9	3553
Kallikrein	MLLRLSEPA	122	9	3554

Table XIV
Prostate B62 Supermotifs with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSA	MLLRLSEPA	118	9	3555
PSA	MLLRLSEPAEL	118	11	3556
Kallikrein	MLLRLSEPAKI	122	11	3557
PAP	MLPGCSPSCPL	343	11	3558
PSM	MMNDQLMF	663	8	3559
PSM	MMNDQLMFL	663	9	3560
PSM	MPEGDLVY	169	8	3561
PSM	MPEGDLVYV	169	9	3562
PSM	MPEGDLVYVNY	169	11	3563
PSM	MVFELANSI	583	9	3564
PSM	MVFELANSIV	583	10	3565
PSM	MVFELANSIVL	583	11	3566
PSM	NIKKFLYNF	69	9	3567
PSM	NILNLNGA	257	8	3568
PSM	NITPKHNM	51	8	3569
PSM	NITPKHNMKA	51	10	3570
PSM	NITPKHNMKAF	51	11	3571
PAP	NLAALPPEGV	119	11	3572
PSM	NLLHETDSA	3	9	3573
PSM	NLLHETDSAV	3	10	3574
PSM	NLLHETDSAVA	3	11	3575
PSM	NLNGAGDPL	260	9	3576
PSM	NMKAFLDEL	57	9	3577
PSM	NMKAFLDELKA	57	11	3578
Kallikrein	NMSLLKHQSL	102	10	3579
PAP	NPILLWQPI	133	9	3580
PAP	NPILLWQPIPV	133	11	3581
PSM	NPIVLRMM	657	8	3582
PSM	NVGPGFTGNF	328	10	3583
PSM	NVIGTLRGA	357	9	3584
PSM	NVIGTLRGAV	357	10	3585
PSM	NVSDIVPPF	153	9	3586
PSM	NVSDIVPPFSA	153	11	3587
PAP	PIDTFPTDPI	49	10	3588
PSM	PIGYYDAQKL	296	10	3589
PSM	PIGYYDAQKLL	296	11	3590
PAP	PIKESSWPQGF	57	11	3591
PAP	PILLWQPI	134	8	3592
PAP	PILLWQPIPV	134	10	3593
PAP	PIPVHTVPL	140	9	3594
PSM	PIVLRMMNDQL	658	11	3595
PAP	PLERFAEL	352	8	3596
PAP	PLERFAELV	352	9	3597
PSM	PLGLPDRPF	678	9	3598

Table XIV
Prostate HLA Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	PLGLPDRPFY	678	10	3599
PSA	PLILSRIV	15	8	3600
PSA	PLILSRIVGGW	15	11	3601
Kallikrein	PLIQSRIV	19	8	3602
Kallikrein	PLIQSRIVGGW	19	11	3603
PAP	PLLLARAA	5	8	3604
PAP	PLLLARAASL	5	10	3605
PSM	PLMYSLVHNL	468	10	3606
PAP	PLSEDQLL	147	8	3607
PAP	PLSEDQLLY	147	9	3608
PAP	PLSEDQLLYL	147	10	3609
PSM	PLTPGYPA	267	8	3610
PSM	PLTPGYPANEY	267	11	3611
Kallikrein	PLVCNGVL	216	8	3612
PSA	PLVCNGVL	212	8	3613
Kallikrein	PLVCNGVLQGI	216	11	3614
PSA	PLVCNGVLQGI	212	11	3615
PAP	PLYCESVHNF	212	10	3616
PSA	PLYDMSLL	95	8	3617
PSM	PLYHSVYETY	550	10	3618
Kallikrein	PLYNMSLL	99	8	3619
PSM	PMFKYHLTV	568	9	3620
PSM	PMFKYHLTVA	568	10	3621
PSM	PPDSSWRGSL	314	10	3622
PAP	PPEGVSIW	125	8	3623
PAP	PPEGVSIWNPI	125	11	3624
PSM	PPFSAFSPQGM	159	11	3625
PSM	PPGYENVSDI	148	10	3626
PSM	PPGYENVSDIV	148	11	3627
PSM	PPPGYENV	147	8	3628
PSM	PPPGYENVSDI	147	11	3629
PSM	PPPPGYENV	146	9	3630
PAP	PPYASCHL	308	8	3631
PAP	PPYASCHLTEL	308	11	3632
PAP	PQDWSTECM	365	9	3633
PSM	PQEMKTYSV	619	9	3634
PSM	PQEMKTYSVSF	619	11	3635
PAP	PQGFGQLTQL	64	10	3636
PSM	PQGMPEGDL	166	9	3637
PSM	PQGMPEGDLV	166	10	3638
PSM	PQGMPEGDLVY	166	11	3639
PSA	PQKVTKFM	185	8	3640
PSA	PQKVTKFML	185	9	3641
PSA	PQKVTKFMLCA	185	11	3642

Table XIV

CTL Prostate H62 SuperMotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	PQSGAAVV	388	8	3643
PSM	PQSGAAVVHEI	388	11	3644
Kallikrein	PQWVLTAA	57	8	3645
PSA	PQWVLTAA	53	8	3646
PSA	PQWVLTAAHCI	53	11	3647
Kallikrein	PQWVLTAAHCL	57	11	3648
PSM	PVHPIGYY	293	8	3649
PSM	PVHPIGYYDA	293	10	3650
Kallikrein	PVSHSFPHPL	91	10	3651
Kallikrein	PVSHSFPHPLY	91	11	3652
PAP	QIPSYKKL	276	8	3653
PAP	QIPSYKKLI	276	9	3654
PAP	QIPSYKKLIM	276	10	3655
PAP	QIPSYKKLIMY	276	11	3656
PSM	QIQSQWKEF	95	9	3657
PSM	QIQSQWKEFGL	95	11	3658
PSM	QIYVAAFTV	731	9	3659
PSM	QIYVAAFTVQA	731	11	3660
PSM	QLAGAKGV	218	8	3661
PSM	QLAGAKGVI	218	9	3662
PSM	QLAGAKGVIL	218	10	3663
PSM	QLAGAKGVILY	218	11	3664
PSM	QLAKQIQSQW	91	10	3665
PAP	QLGMEQHY	72	8	3666
PAP	QLGMEQHYEL	72	10	3667
PSM	QLMFLERA	667	8	3668
PSM	QLMFLERAF	667	9	3669
PSM	QLMFLERAFI	667	10	3670
PAP	QLTQLGMEQHY	69	11	3671
PAP	QMALDVYNGL	297	10	3672
PAP	QMALDVYNGLL	297	11	3673
PAP	QPIPVHTV	139	8	3674
PAP	QPIPVHTVPL	139	10	3675
Kallikrein	QPWQVAVY	36	8	3676
PSA	QPWQVLVA	32	8	3677
Kallikrein	QVAVYSHGW	39	9	3678
Kallikrein	QVAVYSHGWA	39	10	3679
PSA	QVFQVSHSF	84	9	3680
PSA	QVHPQKVTKF	182	10	3681
PSA	QVHPQKVTKFM	182	11	3682
PSA	QVLVASRGRA	35	10	3683
PSA	QVLVASRGRAV	35	11	3684
PSM	QVRGGMVF	578	8	3685
PSM	QVRGGMVFEL	578	10	3686

Table XIV

Prostate 362 Supermotifs with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	QVRGGMVFELA	578	11	3687
PSA	QVSHSFPHPL	87	10	3688
PSA	QVSHSFPHPLY	87	11	3689
Kallikrein	QVWLGRHNL	72	9	3690
Kallikrein	QVWLGRHNLF	72	10	3691
PAP	QVYIRSTDV	101	9	3692
PSM	RISKLGSGNDF	511	11	3693
PSM	RIYNVIGTL	354	9	3694
PSM	RLGIASGRA	527	9	3695
PSM	RLGIASGRARY	527	11	3696
PAP	RLHPYKDF	180	8	3697
PAP	RLHPYKDFI	180	9	3698
PAP	RLHPYKDFIA	180	10	3699
PSM	RLLQERGV	440	8	3700
PSM	RLLQERGVA	440	9	3701
PSM	RLLQERGVAY	440	10	3702
PSM	RLLQERGVAYI	440	11	3703
PSM	RLQDFDKSNPI	649	11	3704
PAP	RLQGGVLV	257	8	3705
PAP	RLQGGVLVNEI	257	11	3706
PSA	RLSEPAEL	121	8	3707
PSA	RLSEPAELTDA	121	11	3708
Kallikrein	RLSEPAKI	125	8	3709
Kallikrein	RLSEPAKITDV	125	11	3710
PSM	RMMNDQLM	662	8	3711
PSM	RMMNDQLMF	662	9	3712
PSM	RMMNDQLMFL	662	10	3713
Kallikrein	RPDEDSSHDL	112	10	3714
Kallikrein	RPDEDSSHDLM	112	11	3715
PSM	RPFYRHVI	684	8	3716
PSM	RPFYRHVIY	684	9	3717
PSM	RPFYRHVIYA	684	10	3718
PSA	RPGDDSSHDL	108	10	3719
PSA	RPGDDSSHDLM	108	11	3720
PSM	RPRRTILF	411	8	3721
PSM	RPRRTILFA	411	9	3722
PSM	RPRRTILFASW	411	11	3723
Kallikrein	RPRSLQCV	167	8	3724
Kallikrein	RPRSLQCVSL	167	10	3725
PSM	RPRWLCAGA	17	9	3726
PSM	RPRWLCAGAL	17	10	3727
PSM	RPRWLCAGALV	17	11	3728
PSA	RPSLYTKV	235	8	3729
PSA	RPSLYTKVV	235	9	3730

Table XIV

Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSA	RPSLYTKVVHY	235	11	3731
PSM	RQIYVAAF	730	8	3732
PSM	RQIYVAAFTV	730	10	3733
PSM	RVDCTPLM	463	8	3734
PSM	RVDCTPLMY	463	9	3735
PSM	RVDCTPLMYSL	463	11	3736
Kallikrein	RVPVSHSF	89	8	3737
Kallikrein	SIALSVGCTGA	7	11	3738
PSM	SIEGNYTL	455	8	3739
PSM	SIEGNYTLRV	455	10	3740
Kallikrein	SIEPEEFL	159	8	3741
PSA	SIEPEEFL	155	8	3742
PSM	SIINEDGNEI	129	10	3743
PSM	SIINEDGNEIF	129	11	3744
PSM	SIPVHPIGY	291	9	3745
PSM	SIPVHPIGYY	291	10	3746
PSM	SISMKHPQEM	613	10	3747
PSM	SIVLPFDCRDY	590	11	3748
PAP	SIWNPILL	130	8	3749
PAP	SIWNPILLW	130	9	3750
PSM	SLFEPPPPGY	142	10	3751
PSA	SLFHPEDTGQV	75	11	3752
PSM	SLFSAVKNF	631	9	3753
PAP	SLGFLFLL	15	8	3754
PAP	SLGFLFLLF	15	9	3755
PAP	SLGFLFLLFF	15	10	3756
PAP	SLGFLFLLFFW	15	11	3757
Kallikrein	SLHLLSNDM	175	9	3758
Kallikrein	SLHLLSNDMCA	175	11	3759
PSM	SLKVPYNV	322	8	3760
Kallikrein	SLLKHQSL	104	8	3761
PSA	SLLKNRFL	100	8	3762
PAP	SLLSLYGI	242	8	3763
Kallikrein	SLQCVSLHL	170	9	3764
Kallikrein	SLQCVSLHLL	170	10	3765
PAP	SLSLGFLF	13	8	3766
PAP	SLSLGFLFL	13	9	3767
PAP	SLSLGFLFLL	13	10	3768
PAP	SLSLGFLFLLF	13	11	3769
PSM	SLVHNLTKEL	472	10	3770
PSA	SLYTKVVHY	237	9	3771
PSM	SMKHPQEM	615	8	3772
PSM	SMKHPQEMKTY	615	11	3773
PSM	SPDEGFEGKSL	483	11	3774

Table XIV
Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	SPEFSGMPRI	503	10	3775
PAP	SPIDTFPTDPI	48	11	3776
PSM	SPQGMPEGDL	165	10	3777
PSM	SPQGMPEGDLV	165	11	3778
PAP	SPSCPLERF	348	9	3779
PAP	SPSCPLERFA	348	10	3780
PSM	SPSPEFSGM	501	9	3781
Kallikrein	SQPWQVAV	35	8	3782
Kallikrein	SQPWQVAVY	35	9	3783
PSA	SQPWQVLV	31	8	3784
PSA	SQPWQVLVA	31	9	3785
Kallikrein	SQVWLGRHNL	71	10	3786
Kallikrein	SQVWLGRHNLF	71	11	3787
PSM	SQWKEFGL	98	8	3788
PSM	SQWKEFGLDSV	98	11	3789
PSM	SVELAHYDV	107	9	3790
PSM	SVELAHYDVL	107	10	3791
PSM	SVELAHYDVLL	107	11	3792
Kallikrein	SVGCTGAV	11	8	3793
Kallikrein	SVGCTGAVPL	11	10	3794
Kallikrein	SVGCTGAVPLI	11	11	3795
PAP	SVHNFTLPSW	217	10	3796
PAP	SVHNFTLPSWA	217	11	3797
PSA	SVILLGRHSL	67	10	3798
PSA	SVILLGRHSLF	67	11	3799
PAP	SVLAKELKF	29	9	3800
PAP	SVLAKELKFV	29	10	3801
PSM	SVSFDSLF	626	8	3802
PSM	SVSFDSLFSA	626	10	3803
PSM	SVSFDSLFSAV	626	11	3804
PSA	SVTWIGAA	7	8	3805
PSA	SVTWIGAAPL	7	10	3806
PSA	SVTWIGAAPLI	7	11	3807
PSM	SVYETYEL	554	8	3808
PSM	SVYETYELV	554	9	3809
PSM	TILFASWDA	415	9	3810
PAP	TLGKLSGL	190	8	3811
PAP	TLKSEEFQKRL	171	11	3812
PAP	TLMSAMTNL	112	9	3813
PAP	TLMSAMTNLA	112	10	3814
PAP	TLMSAMTNLAA	112	11	3815
PAP	TLPSWATEDTM	222	11	3816
PSM	TLRGAVEPDRY	361	11	3817
PSM	TLRVDCTPL	461	9	3818

Table XIV

Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	TLRVDCTPLM	461	10	3819
PSM	TLRVDCTPLMY	461	11	3820
PSA	TLSVTWIGA	5	9	3821
PSA	TLSVTWIGAA	5	10	3822
PAP	TMTKLREL	231	8	3823
PAP	TMTKLRELSEL	231	11	3824
PSM	TPGYPANEY	269	9	3825
PSM	TPGYPANEYA	269	10	3826
PSM	TPGYPANEYAY	269	11	3827
PSM	TPKHNMKA	53	8	3828
PSM	TPKHNMKAF	53	9	3829
PSM	TPKHNMKAFL	53	10	3830
PSA	TPKKLQCV	163	8	3831
PSA	TPKKLQCVDL	163	10	3832
PSM	TPLMYSLV	467	8	3833
PSM	TPLMYSLVHNL	467	11	3834
Kallikrein	TQEPALGTTCY	143	11	3835
PSA	TQEPALGTTCY	139	11	3836
PAP	TQHEPYPL	335	8	3837
PAP	TQHEPYPLM	335	9	3838
PAP	TQHEPYPLML	335	10	3839
PAP	TQIPSYKKL	275	9	3840
PAP	TQIPSYKKLI	275	10	3841
PAP	TQIPSYKKLIM	275	11	3842
PSM	TQKVKMHI	339	8	3843
PAP	TQLGMEQHY	71	9	3844
PAP	TQLGMEQHYEL	71	11	3845
PSM	TVAQVRGGM	575	9	3846
PSM	TVAQVRGGMV	575	10	3847
PSM	TVAQVRGGMVF	575	11	3848
PAP	TVPLSEDQL	145	9	3849
PAP	TVPLSEDQLL	145	10	3850
PAP	TVPLSEDQLLY	145	11	3851
PSM	TVQAAAETL	738	9	3852
PAP	TVSGLQMA	292	8	3853
PAP	TVSGLQMAL	292	9	3854
PAP	TVSGLQMALDV	292	11	3855
PSM	VIARYGKV	201	8	3856
PSM	VIARYGKVF	201	9	3857
PSM	VIGTLRGA	358	8	3858
PSM	VIGTLRGAV	358	9	3859
PSM	VILGGHRDSW	372	10	3860
PSM	VILGGHRDSWV	372	11	3861
PSA	VILLGRHSL	68	9	3862

Table XIV
Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSA	VILLGRHSLF	68	10	3863
PSM	VILYSDPA	225	8	3864
PSM	VILYSDPADY	225	10	3865
PSM	VILYSDPADYF	225	11	3866
PAP	VIPQDWSTECM	363	11	3867
PSA	VISNDVCA	174	8	3868
PSA	VISNDVCAQV	174	10	3869
PSM	VIYAPSSHNKY	690	11	3870
PSM	VLAGGFFL	27	8	3871
PSM	VLAGGFFLL	27	9	3872
PSM	VLAGGFFLLGF	27	11	3873
PAP	VLAKELKF	30	8	3874
PAP	VLAKELKFV	30	9	3875
PAP	VLAKELKFVTL	30	11	3876
Kallikrein	VLGLPTQEPA	138	10	3877
Kallikrein	VLGLPTQEPAL	138	11	3878
PSM	VLPFDCRDY	592	9	3879
PSM	VLPFDCRDYA	592	10	3880
PSM	VLPFDCRDYAV	592	11	3881
Kallikrein	VLQGITSW	222	8	3882
PSA	VLQGITSW	218	8	3883
PSM	VLRKYADKI	603	9	3884
PSM	VLRKYADKIY	603	10	3885
PSM	VLRMMNDQL	660	9	3886
PSM	VLRMMNDQLM	660	10	3887
PSM	VLRMMNDQLMF	660	11	3888
Kallikrein	VLSIALSV	5	8	3889
PSA	VLTAAHCI	56	8	3890
Kallikrein	VLTAAHCL	60	8	3891
PSA	VLVASRGRA	36	9	3892
PSA	VLVASRGRAV	36	10	3893
Kallikrein	VLVHPQWV	53	8	3894
PSA	VLVHPQWV	49	8	3895
Kallikrein	VLVHPQWVL	53	9	3896
PSA	VLVHPQWVL	49	9	3897
Kallikrein	VLVHPQWVLTA	53	11	3898
PSA	VLVHPQWVLTA	49	11	3899
PAP	VLVNEILNHM	262	10	3900
PSA	VMDLPTQEPA	134	10	3901
PSA	VMDLPTQEPAL	134	11	3902
Kallikrein	VPLIQSRI	18	8	3903
Kallikrein	VPLIQSRIV	18	9	3904
PAP	VPLSEDQL	146	8	3905
PAP	VPLSEDQLL	146	9	3906

Table XIV
Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PAP	VPLSEDQLLY	146	10	3907
PAP	VPLSEDQLLYL	146	11	3908
Kallikrein	VPVSHSFPHPL	90	11	3909
PSM	VPYNVGPGF	325	9	3910
PSM	VQAAAETL	739	8	3911
PSM	VQAAAETLSEV	739	11	3912
PSM	VQRGNILNL	253	9	3913
PSA	VVFLTLSV	1	8	3914
PSA	VVFLTLSVTW	1	10	3915
PSA	VVFLTLSVTWI	1	11	3916
PSM	VVHEIVRSF	394	9	3917
Kallikrein	VVHYRKWI	246	8	3918
PSA	VVHYRKWI	242	8	3919
PSM	VVLRKYADKI	602	10	3920
PSM	VVLRKYADKIY	602	11	3921
PSA	WIGAAPLI	10	8	3922
PSA	WIGAAPLIL	10	9	3923
Kallikrein	WIKDTIAA	252	8	3924
PSA	WIKDTIVA	248	8	3925
PSM	WLCAGALV	20	8	3926
PSM	WLCAGALVL	20	9	3927
PSM	WLCAGALVLA	20	10	3928
PAP	WLDRSVLA	25	8	3929
PAP	WLDRSVLAKEL	25	11	3930
Kallikrein	WLGRHNLF	74	8	3931
PAP	WPQGFGQL	63	8	3932
PAP	WPQGFGQLTQL	63	11	3933
PAP	WQPIPVHTV	138	9	3934
PAP	WQPIPVHTVPL	138	11	3935
Kallikrein	WQVAVYSHGW	38	10	3936
Kallikrein	WQVAVYSHGWA	38	11	3937
PSA	WQVLVASRGRA	34	11	3938
PSA	WVLTAAHCI	55	9	3939
Kallikrein	WVLTAAHCL	59	9	3940
PSM	YINADSSI	449	8	3941
PAP	YIRKRYRKF	84	9	3942
PAP	YIRKRYRKFL	84	10	3943
PAP	YIRSTDVDRTL	103	11	3944
PAP	YLPFRNCPRF	155	10	3945
PSM	YPANEYAY	272	8	3946
PSM	YPLYHSVY	549	8	3947
PSM	YPLYHSVYETY	549	11	3948
PSM	YPNKTHPNY	119	9	3949
PSM	YPNKTHPNYI	119	10	3950

Table XIV
HLA-A1 Prostate B62 Supermotif with Binding Data

Protein	Sequence	Position	No. of Amino Acids	Seq. Id. No.
PSM	YVAAFTVQA	733	9	3951
PSM	YVAAFTVQAA	733	10	3952
PSM	YVAAFTVQAAA	733	11	3953
PSM	YVILGGHRDSW	371	11	3954
PSM	YVNYARTEDF	176	10	3955
PSM	YVNYARTEDFF	176	11	3956

Table XV

Prostate A01 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0101	Seq. Id. No.
PSM	ADSSIEGNY	452	9		3957
PSM	AGAKGVILY	220	9		3958
PSM	AGDPLTPGY	264	9	0.0099	3959
PSM	AGESFPGIY	701	9	0.0040	3960
PSM	APSSHNKY	693	8		3961
PAP	ASCHLTELY	311	9	0.7700	3962
PSM	CRDYAVVLRKY	597	11		3963
PSM	CSGKIVIARY	196	10	0.0160	3964
PSM	DSSIEGNY	453	8		3965
PSM	DSVELAHY	106	8		3966
PSM	DYAVVLRKY	599	9		3967
PSM	EGDLVYVNY	171	9	0.0024	3968
PSM	ELAHYDVLLSY	109	11		3969
PAP	ELSELSLLSLY	237	11		3970
PAP	ELSLLSLY	240	8		3971
Kallikrein	EPALGTTCY	145	9	0.0011	3972
PSA	EPALGTTCY	141	9	0.0011	3973
PAP	ESYKHEQVY	95	9	0.0980	3974
PSM	ETNKFSGY	542	8		3975
PSM	ETNKFSGYPLY	542	11		3976
PSM	ETYELVEKFY	557	10	0.0260	3977
PSM	FSGYPLYHSVY	546	11		3978
PSM	FYDPMFKY	565	8		3979
PSM	GESFPGIY	702	8		3980
PSM	GFEGKSLY	487	8		3981
PSM	GIASGRARY	529	9	0.0025	3982
PSM	GLDSVELAHY	104	10	0.4800	3983
PAP	GMEQHYELGEY	74	11		3984
PSM	GMPEGDLVY	168	9	0.0001	3985
PAP	HMKRATQIPSY	270	11		3986
Kallikrein	HSFPHPLY	94	8	0.0260	3987
PSA	HSFPHPLY	90	8	0.0260	3988
Kallikrein	HSQPWQVAVY	34	10		3989
PSM	HSTNEVTRIY	347	10	0.0048	3990
PSM	HYDVLLSY	112	8		3991
PSM	IASGRARY	530	8		3992
PSM	IHSTNEVTRIY	346	11		3993
PSM	INADSSIEGNY	450	11		3994
PAP	IPSYKKLIMY	277	10	0.5700	3995
PAP	IWSKVYDPLY	205	10	0.0012	3996
PSM	IYAPSSHNKY	691	10		3997
PSM	KAENIKKFLY	66	10	0.0001	3998
PSM	KFSGYPLY	545	8		3999
PAP	KGEYFVEMY	322	9	3.4000	4000
PAP	KGEYFVEMYY	322	10	0.0180	4001
Kallikrein	KHSQPWQVAVY	33	11		4002

Table XV

Prostate 600 Mer Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0101	Seq. Id. No.
Kallikrein	KPAVYTKVVHY	239	11		4003
PAP	KRATQIPSY	272	9	0.0011	4004
PSM	KYAGESFPGIY	699	11		4005
PSM	LDSVELAHY	105	9		4006
PSM	LFEPPPPGY	143	9	0.0010	4007
PAP	LGEYIRKRY	81	9	0.7800	4008
PSM	LKAENIKKFLY	65	11		4009
Kallikrein	LLSNDMCARAY	178	11		4010
PAP	LNESYKHEQVY	93	11		4011
Kallikrein	LPEKPAVY	236	8		4012
PSA	LPERPSLY	232	8	0.0002	4013
PSM	LPSIPVHPIGY	289	11		4014
PSM	LQERGVAY	442	8		4015
PAP	LSEDQLLY	148	8		4016
PAP	LSELSLLSLY	238	10	12.0000	4017
Kallikrein	LSNDMCARAY	179	10		4018
PSM	LSYPNKTHPNY	117	11		4019
PAP	LTELYFEKGEY	315	11		4020
PSM	LTPGYPANEY	268	10	0.0082	4021
PAP	LTQLGMEQHY	70	10	0.6200	4022
PSM	LYSDPADY	227	8		4023
PSM	MPEGDLVY	169	8		4024
PSM	MPEGDLVYVNY	169	11		4025
PSM	NADSSIEGNY	451	10	0.4300	4026
PSM	NCSGKIVIARY	195	11		4027
PAP	NESYKHEQVY	94	10	0.0033	4028
PSM	NGAGDPLTPGY	262	11		4029
PSM	NWETNKFSGY	540	10		4030
Kallikrein	PCALPEKPAVY	233	11		4031
PSA	PCALPERPSLY	229	11		4032
PSM	PDEGFEGKSLY	484	11		4033
PAP	PLSEDQLLY	147	9	1.2000	4034
PSM	PSIPVHPIGY	290	10		4035
PSM	PSIPVHPIGYY	290	11		4036
PSA	PSLYTKVVHY	236	10	0.0010	4037
PAP	PSYKKLIMY	278	9	0.0031	4038
Kallikrein	PVSHSFPHPLY	91	11		4039
PAP	PYASCHLTELY	309	11		4040
PSM	QLAGAKGVILY	218	11		4041
PSA	QVSHSFPHPLY	87	11		4042
PSM	RGAVEPDRY	363	9	0.0001	4043
PSM	RGSLKVPY	320	8		4044
PAP	RNETQHEPY	332	9	0.0002	4045
PSA	RPSLYTKVVHY	235	11		4046
PSM	RVDCTPLMY	463	9	11.0000	4047
PAP	SEEFQKRLHPY	174	11		4048

Table XV
Prostate A01 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0101	Seq. Id. No.
Kallikrein	SHSFPHPLY	93	9	0.0011	4049
PSA	SHSFPHPLY	89	9	0.0011	4050
PSM	SMKHPQEMKTY	615	11		4051
Kallikrein	SNDMCARAY	180	9		4052
PSM	SSWRGSLKVPY	317	11		4053
PSM	STNEVTRIY	348	9	0.0430	4054
PSM	TNEVTRIY	349	8		4055
Kallikrein	TQEPALGTTCY	143	11	0.0190	4056
PSA	TQEPALGTTCY	139	11	0.0190	4057
PSM	TSLFEPPPPGY	141	11		4058
PSM	TYELVEKFY	558	9	0.0010	4059
PAP	VSGLQMALDVY	293	11		4060
Kallikrein	VSHSFPHPLY	92	10	0.1500	4061
PSA	VSHSFPHPLY	88	10	0.1500	4062
PSM	WGEVKRQIY	725	9	0.0010	4063
PAP	WSKVYDPLY	206	9	0.0046	4064
PAP	YASCHLTELY	310	10	0.5500	4065
PSM	YFAPGVKSY	234	9		4066
PSM	YHSVYETY	552	8		4067
PSM	YPANEYAY	272	8		4068

Table XVI

Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSM	AAAETLSEVA	741	10		4069
PSM	AAETLSEVA	742	9		4070
PSM	AAFTVQAA	735	8		4071
PSM	AAFTVQAAA	735	9		4072
PSA	AAHCIRNK	59	8		4073
PSA	AAPLILSR	13	8		4074
PAP	AAPLLLAR	3	8		4075
PAP	AAPLLLARA	3	9		4076
PAP	AAPLLLARAA	3	10		4077
PAP	AASLSLGF	11	8		4078
PAP	AASLSLGFLF	11	10		4079
PSM	AAVVHEIVR	392	9		4080
PSM	AAVVHEIVRSF	392	11		4081
PSM	ADKIYSISMK	608	10		4082
PSM	ADKIYSISMKH	608	11		4083
PSM	ADSSIEGNY	452	9		4084
PSM	ADYFAPGVK	232	9	0.0006	4085
PSM	ADYFAPGVKSY	232	11		4086
PSM	AFIDPLGLPDR	674	11		4087
PSM	AFLDELKA	60	8		4088
PSM	AFTVQAAA	736	8		4089
PSM	AGAKGVILY	220	9		4090
PSM	AGALVLAGGF	23	10		4091
PSM	AGALVLAGGFF	23	11		4092
PSM	AGDPLTPGY	264	9		4093
PSM	AGDPLTPGYPA	264	11		4094
PSM	AGESFPGIY	701	9		4095
PSM	AGESFPGIYDA	701	11		4096
PSM	AGGFFLLGF	29	9		4097
PSM	AGGFFLLGFLF	29	11		4098
Kallikrein	AGLWTGGK	199	8		4099
PSA	AGRWTGGK	195	8		4100
PSM	AGTEQNFQLA	84	10		4101
PSM	AGTEQNFQLAK	84	11		4102
PSM	ALFDIESK	711	8		4103
Kallikrein	ALGTTCYA	147	8		4104
PSA	ALGTTCYA	143	8		4105
Kallikrein	ALPEKPAVY	235	9		4106
Kallikrein	ALPEKPAVYTK	235	11		4107
PSA	ALPERPSLY	231	9	0.0170	4108
PSA	ALPERPSLYTK	231	11		4109
Kallikrein	ALSVGCTGA	9	9		4110
PSM	ALVLAGGF	25	8		4111
PSM	ALVLAGGFF	25	9		4112
PAP	AMTNLAALF	116	9		4113
PAP	ASCHLTELY	311	9	0.0002	4114

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PAP	ASCHLTELYF	311	10		4115
PSM	ASGRARYTK	531	9	0.0086	4116
PSM	ASKESERLQDF	643	11		4117
PAP	ASLSLGFLF	12	9		4118
PSM	ASWDAEEF	419	8		4119
PSM	ATARRPRWLCA	13	11		4120
PAP	ATEDTMTK	227	8	0.0003	4121
PAP	ATEDTMTKLR	227	10		4122
PAP	ATLGKLSGLH	189	10		4123
PSM	ATNITPKH	49	8		4124
PSM	ATNITPKHNMK	49	11		4125
PAP	ATQIPSYK	274	8	0.0180	4126
PAP	ATQIPSYKK	274	9	0.1000	4127
PSM	AVATARRPR	11	9		4128
PSA	AVCGGVLVH	44	9		4129
PSM	AVGLPSIPVH	286	10		4130
PSM	AVKNFTEIA	635	9		4131
PSM	AVKNFTEIASK	635	11		4132
Kallikrein	AVPLIQSR	17	8		4133
PSM	AVVHEIVR	393	8		4134
PSM	AVVHEIVRSF	393	10		4135
PSM	AVVLRKYA	601	8		4136
PSM	AVVLRKYADK	601	10	0.0026	4137
Kallikrein	AVYSHGWA	41	8		4138
Kallikrein	AVYSHGWAH	41	9		4139
Kallikrein	AVYTKVVH	241	8		4140
Kallikrein	AVYTKVVHY	241	9		4141
Kallikrein	AVYTKVVHYR	241	10		4142
Kallikrein	AVYTKVVHYRK	241	11		4143
PSM	CAGALVLA	22	8		4144
PSM	CAGALVLAGGF	22	11		4145
Kallikrein	CAGLWTGGK	198	9		4146
PSA	CAGRWTGGK	194	9	0.0006	4147
Kallikrein	CALPEKPA	234	8		4148
Kallikrein	CALPEKPAVY	234	10		4149
PSA	CALPERPSLY	230	10		4150
PSA	CAQVHPQK	180	8		4151
PSA	CAQVHPQKVTK	180	11		4152
Kallikrein	CARAYSEK	184	8		4153
PSM	CSGKIVIA	196	8		4154
PSM	CSGKIVIAR	196	9		4155
PSM	CSGKIVIARY	196	10	0.0600	4156
PAP	CSPSCPLER	347	9	0.0040	4157
PAP	CSPSCPLERF	347	10		4158
PAP	CSPSCPLERFA	347	11		4159
Kallikrein	CTGAVPLIQSR	14	11		4160

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSM	CTPLMYSLVH	466	10		4161
PSM	DALFDIESK	710	9	0.0006	4162
PSM	DAQKLLEK	301	8		4163
PSM	DCRDYAVVLR	596	10		4164
PSM	DCRDYAVVLRK	596	11		4165
PSM	DCTPLMYSLVH	465	11		4166
PSA	DDSSHDLMLLR	111	11		4167
PSM	DFDKSNPIVLR	652	11		4168
PSM	DFEVFFQR	520	8		4169
PSM	DFFKLERDMK	184	10		4170
PAP	DFIATLGK	186	8		4171
PSM	DGNEIFNTSLF	134	11		4172
PSM	DIESKVDPSK	714	10	0.0003	4173
PSM	DIESKVDPSKA	714	11		4174
PSM	DIVPPFSA	156	8		4175
PSM	DIVPPFSAF	156	9		4176
PAP	DLFGIWSK	201	8		4177
PAP	DLFGIWSKVY	201	10		4178
PSA	DLHVISNDVCA	171	11		4179
Kallikrein	DLMLLRLSEPA	120	11		4180
PSA	DLMLLRLSEPA	116	11		4181
PSA	DLPTQEPA	136	8		4182
PSM	DLVYVNYA	173	8		4183
PSM	DLVYVNYAR	173	9		4184
Kallikrein	DMCARAYSEK	182	10		4185
PSM	DMKINCSGK	191	9		4186
PSA	DMSLLKNR	98	8	0.0003	4187
PSA	DMSLLKNRF	98	9		4188
PSA	DMSLLKNRFLR	98	11		4189
PSM	DSAVATAR	9	8		4190
PSM	DSAVATARR	9	9		4191
PSM	DSAVATARRPR	9	11		4192
PSM	DSLFSAVK	630	8		4193
PSM	DSLFSAVKNF	630	10		4194
Kallikrein	DSSHDLMLLR	116	10		4195
PSA	DSSHDLMLLR	112	10		4196
PSM	DSSIEGNY	453	8		4197
PSM	DSSIEGNYTLR	453	11		4198
PSM	DSSWRGSLK	316	9	0.0032	4199
PSM	DSVELAHY	106	8		4200
PAP	DTFPTDPIK	51	9	0.0001	4201
Kallikrein	DTGQRVPVSH	85	10		4202
PSA	DTGQVFQVSH	81	10		4203
PAP	DTTVSGLQMA	290	10		4204
PSA	DVCAQVHPQK	178	10	0.0007	4205
PAP	DVDRTLMSA	108	9		4206

Table XVI

Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSM	DVLLSYPNK	114	9	0.0006	4207
PSM	DVLLSYPNKTH	114	11		4208
PAP	DVYNGLLPPY	301	10		4209
PAP	DVYNGLLPPYA	301	11		4210
PSM	EATNITPK	48	8		4211
PSM	EATNITPKH	48	9		4212
PSM	EAVGLPSIPVH	285	11		4213
PAP	ECMTTNSH	371	8		4214
PSM	EDFFKLER	183	8		4215
PSM	EDFFKLERDMK	183	11		4216
PAP	EDQLLYLPF	150	9		4217
PAP	EDQLLYLPFR	150	10		4218
Kallikrein	EDSSHDLMLLR	115	11		4219
Kallikrein	EDTGQRVPVSH	84	11		4220
PSA	EDTGQVFQVSH	80	11		4221
PAP	EDTMTKLR	229	8		4222
PSM	EFGLDSVELA	102	10		4223
PSM	EFGLDSVELAH	102	11		4224
PSM	EFGLLGSTEWA	425	11		4225
PAP	EFQKRLHPY	176	9		4226
PAP	EFQKRLHPYK	176	10		4227
PSM	EFSGMPRISK	505	10		4228
PSM	EGDLVYVNY	171	9		4229
PSM	EGDLVYVNYA	171	10		4230
PSM	EGDLVYVNYAR	171	11		4231
PSM	EGFEGKSLY	486	9		4232
PSM	EGKSLYESWTK	489	11		4233
PSM	EGWRPRRTILF	408	11		4234
PSM	EIASKFSER	641	9	0.0006	4235
PSM	EIFNTSLF	137	8		4236
PAP	EILNHMKR	266	8		4237
PAP	EILNHMKRA	266	9		4238
PSM	EIVRSFGTLK	397	10		4239
PSM	EIVRSFGTLKK	397	11		4240
PSM	ELAHYDVLLSY	109	11		4241
PSM	ELANSIVLPF	586	10		4242
PAP	ELESETLK	166	8		4243
PAP	ELGEYIRK	80	8		4244
PAP	ELGEYIRKR	80	9		4245
PAP	ELGEYIRKRY	80	10		4246
PAP	ELGEYIRKRYR	80	11		4247
PSM	ELKAENIK	64	8		4248
PSM	ELKAENIKK	64	9		4249
PSM	ELKAENIKKF	64	10		4250
PAP	ELKEVTLVF	34	9		4251
PAP	ELKEVTLVFR	34	10	0.0014	4252

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PAP	ELKFVTLVFRH	34	11		4253
PSM	ELKSPDEGF	480	9		4254
PAP	ELSELSLLSLY	237	11		4255
PAP	ELSLLSLY	240	8		4256
PAP	ELSLLSLYGHI	240	11		4257
PSM	ELVEKFYDPMF	560	11		4258
PAP	ELYFEKGEY	317	9		4259
PAP	ELYFEKGEYF	317	10		4260
PSM	EMKTYSVSF	621	9	0.0005	4261
PAP	EMYYRNETQH	328	10		4262
PAP	ESETLKSEEF	168	10		4263
PSM	ESFPGIYDA	703	9		4264
PSM	ESFPGIYDALF	703	11		4265
PSM	ESKVDPSK	716	8		4266
PSM	ESKVDPSKA	716	9		4267
PAP	ESSWPQGF	60	8		4268
PAP	ESYKHEQVY	95	9	0.0002	4269
PAP	ESYKHEQVYIR	95	11		4270
PSM	ETDSAVATA	7	9		4271
PSM	ETDSAVATAR	7	10		4272
PSM	ETDSAVATARR	7	11		4273
PAP	ETLKSEEF	170	8		4274
PAP	ETLKSEEFQK	170	10	0.0004	4275
PAP	ETLKSEEFQKR	170	11		4276
PSM	ETNKFSGY	542	8		4277
PSM	ETNKFSGYPLY	542	11		4278
PSM	ETYELVEK	557	8		4279
PSM	ETYELVEKF	557	9		4280
PSM	ETYELVEKFY	557	10	0.0006	4281
PSM	EVFFQRLGIA	522	10		4282
PSM	EVKRQIYVA	727	9		4283
PSM	EVKRQIYVAA	727	10		4284
PSM	EVKRQIYVAAF	727	11		4285
PSM	FAPGVKSY	235	8		4286
PSM	FASWDAEEF	418	9		4287
PSM	FDCRDYAVVLR	595	11		4288
PSM	FDIESKVDPSK	713	11		4289
PSM	FDKSNPIVLR	653	10		4290
PSM	FDSLFSAVK	629	9		4291
PSM	FDSLFSAVKNF	629	11		4292
PSM	FFKLERDMK	185	9		4293
PSM	FFLLGFLF	32	8		4294
PSM	FFLLGFLFGWF	32	11		4295
PSM	FFQRLGIA	524	8		4296
PSM	FFQRLGIASGR	524	11		4297
PAP	FFWLDRSVLA	23	10		4298

Table XVI
Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PAP	FFWLDRSVLAK	23	11		4299
PSM	FGGIDPQSGA	383	10		4300
PSM	FGGIDPQSGAA	383	11		4301
PAP	FGIWSKVY	203	8		4302
PSM	FGLDSVELA	103	9		4303
PSM	FGLDSVELAH	103	10		4304
PSM	FGLDSVELAHY	103	11		4305
PSM	FGLLGSTEWA	426	10		4306
PSM	FGTLKKEGWR	402	10		4307
PSM	FGWFIKSSNEA	39	11		4308
PSM	FIDPLGLPDR	675	10		4309
PSM	FIKSSNEA	42	8		4310
PSM	FLDELKAENIK	61	11		4311
PSM	FLFGWFIK	37	8		4312
PAP	FLFLLFFWLDR	18	11		4313
PAP	FLLFFWLDR	20	9	0.0024	4314
PSM	FLLGFLFGWF	33	10		4315
PAP	FLNESYKH	92	8		4316
PSA	FLRPGDDSSH	106	10		4317
PSA	FLTLSVTWIGA	3	11		4318
PSM	FLYNFTQIPH	73	10	0.0102	4319
PSM	FSAVKNFTEIA	633	11		4320
PSM	FSERLQDF	646	8		4321
PSM	FSERLQDFDK	646	10	0.0003	4322
PSM	FSGMPRISK	506	9		4323
PSM	FSGYPLYH	546	8		4324
PSM	FSGYPLYHSVY	546	11		4325
PSM	FSTQKVKMH	337	9		4326
PSM	FSTQKVKMHIH	337	11		4327
PSM	FTEIASKF	639	8		4328
PSM	FTEIASKFSER	639	11		4329
PSM	FTGNFSTQK	333	9		4330
PSM	FTGNFSTQKVK	333	11		4331
PSM	FTQIPHLA	77	8		4332
PAP	FVTLVFRH	37	8		4333
PAP	FVTLVFRHGDR	37	11		4334
PSA	GAAPLILSR	12	9	0.0150	4335
PSM	GAAVVHEIVR	391	10		4336
PSM	GAGDPLTPGY	263	10		4337
PSM	GAKGVILY	221	8		4338
PSM	GALVLAGGF	24	9		4339
PSM	GALVLAGGFF	24	10		4340
PSM	GAVEPDRY	364	8		4341
Kallikrein	GAVPLIQSR	16	9		4342
PAP	GCSPSCPLER	346	10		4343
PAP	GCSPSCPLERF	346	11		4344

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSM	GDLVYVNY	172	8		4345
PSM	GDLVYVNYA	172	9		4346
PSM	GDLVYVNYAR	172	10		4347
PSM	GDPLTPGY	265	8		4348
PSM	GDPLTPGYPA	265	10		4349
PAP	GDRSPIDTF	45	9		4350
PSM	GFEGKSLY	487	8		4351
PSM	GFFLLGFLF	31	9	0.0005	4352
PSM	GFLFGWFIK	36	9	0.0007	4353
PAP	GFLFLLFF	17	8		4354
PSM	GFTGNFSTQK	332	10		4355
PSM	GGFFLLGF	30	8		4356
PSM	GGFFLLGFLF	30	10		4357
PSM	GGHRDSWVF	375	9		4358
PSM	GGIDPQSGA	384	9		4359
PSM	GGIDPQSGAA	384	10		4360
PSM	GGMVFELA	581	8		4361
PSM	GGSAPPDSSWR	310	11		4362
PAP	GGVLVNEILNH	260	11		4363
Kallikrein	GGWECEKH	27	8		4364
PSA	GGWECEKH	23	8		4365
PSM	GIASGRAR	529	8		4366
PSM	GIASGRARY	529	9		4367
PSM	GIASGRARYTK	529	11		4368
PSM	GIDPQSGA	385	8		4369
PSM	GIDPQSGAA	385	9		4370
PAP	GIIKQKEK	248	8		4371
PAP	GIIKQKEKSR	248	10		4372
Kallikrein	GITSWGPEPCA	225	11		4373
PSA	GITSWGSEPCA	221	11		4374
PAP	GIWSKVYDPLY	204	11		4375
PSM	GLDSVELA	104	8		4376
PSM	GLDSVELAH	104	9		4377
PSM	GLDSVELAHY	104	10		4378
PAP	GLHGQDLF	196	8		4379
PSM	GLLGSTEWA	427	9		4380
PAP	GLLPPYASCH	305	10		4381
PSM	GLPDRPFY	680	8		4382
PSM	GLPDRPFYR	680	9	0.0460	4383
PSM	GLPDRPFYRH	680	10		4384
PSM	GLPSIPVH	288	8		4385
Kallikrein	GLPTQEPA	140	8		4386
PAP	GLQMALDVY	295	9		4387
PAP	GMEQHYELGEY	74	11		4388
PSM	GMPEGDLVY	168	9	0.0007	4389
PSM	GSAPPDSSWR	311	10	0.0006	4390

Table XVI

Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSA	GSEPCALPER	226	10		4391
PSM	GSGNDFEVF	516	9		4392
PSM	GSGNDFEVFF	516	10		4393
Kallikrein	GSIEPEEF	158	8		4394
PSA	GSIEPEEF	154	8		4395
Kallikrein	GSIEPEEFLR	158	10		4396
PSM	GSTEWAEENSR	430	11		4397
PSM	GTEQNFQLA	85	9		4398
PSM	GTEQNFQLAK	85	10		4399
PSM	GTLKKEGWR	403	9		4400
PSM	GTLKKEGWRPR	403	11		4401
PSM	GTLRGAVEPDR	360	11		4402
PSM	GVILYSDPA	224	9		4403
PSM	GVILYSDPADY	224	11		4404
PAP	GVLVNEILNH	261	10		4405
Kallikrein	HCGGVLVH	49	8		4406
PAP	HDTTVSGLQMA	289	11		4407
PAP	HGDRSPIDTF	44	10		4408
PAP	HGQDLFGIWSK	198	11		4409
PSM	HHISTNEVTR	345	10		4410
PSM	HLAGTEQNF	82	9		4411
Kallikrein	HLLSNDMCA	177	9		4412
Kallikrein	HLLSNDMCAR	177	10		4413
Kallikrein	HLLSNDMCARA	177	11		4414
PAP	HLTELYFEK	314	9	0.2700	4415
PSM	HLTVAQVR	573	8		4416
PAP	HMKRATQIPSY	270	11		4417
Kallikrein	HSFPHPLY	94	8	0.0890	4418
PSA	HSFPHPLY	90	8	0.0890	4419
Kallikrein	HSQPWQVA	34	8		4420
Kallikrein	HSQPWQVAVY	34	10		4421
PSA	HSQPWQVLVA	30	10		4422
PSM	HSTNEVTR	347	8		4423
PSM	HSTNEVTRIY	347	10	0.0005	4424
PSA	HVISNDVCA	173	9		4425
PSM	HVIYAPSSH	689	9		4426
PSM	HVIYAPSSHNK	689	11		4427
Kallikrein	IALSVGCTGA	8	10		4428
PSM	IARYGKVF	202	8		4429
PSM	IARYGKVFR	202	9		4430
PSM	IASGRARY	530	8		4431
PSM	IASGRARYTK	530	10		4432
PSM	IASKFSER	642	8		4433
PAP	IATLGKLSGLH	188	11		4434
PSM	IDPLGLPDR	676	9		4435
PSM	IDPLGLPDRPF	676	11		4436

Table XVI

Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSM	IDPQSGAA	386	8		4437
PSM	IDPQSGAAVVH	386	11		4438
PAP	IDTFPTDPIK	50	10		4439
PSA	IGAAPLILSR	11	10		4440
PSM	IGYYDAQK	297	8		4441
PSM	IINEDGNEIF	130	10		4442
PSM	ILFASWDA	416	8		4443
PSM	ILFASWDAEEF	416	11		4444
PSM	ILGGHRDSWVF	373	11		4445
PSA	ILLGRHSLF	69	9		4446
PSA	ILLGRHSLFH	69	10		4447
PAP	ILLWQPIPVH	135	10		4448
PAP	ILNHMKRA	267	8		4449
PSM	ILYSDPADY	226	9		4450
PSM	ILYSDPADYF	226	10		4451
PSM	ILYSDPADYFA	226	11		4452
PSM	ISKLGSGNDF	512	10		4453
PSM	ISMKHPQEMK	614	10	0.1900	4454
PSA	ISNDVCAQVH	175	10		4455
PSM	ITPKHNMK	52	8		4456
PSM	ITPKHNMKA	52	9		4457
PSM	ITPKHNMKAF	52	10		4458
Kallikrein	ITSWGPEPCA	226	10		4459
PSA	ITSWGSEPCA	222	10		4460
Kallikrein	IVGGWECEK	25	9	0.0410	4461
PSA	IVGGWECEK	21	9	0.0410	4462
Kallikrein	IVGGWECEKH	25	10		4463
PSA	IVGGWECEKH	21	10		4464
PSM	IVIARYGK	200	8		4465
PSM	IVIARYGKVF	200	10		4466
PSM	IVIARYGKVFR	200	11		4467
PSM	IVLPFDCR	591	8		4468
PSM	IVLPFDCRDY	591	10		4469
PSM	IVLPFDCRDYA	591	11		4470
PSM	IVPPFSAF	157	8		4471
PSM	IVRSFGTLK	398	9	0.1700	4472
PSM	IVRSFGTLKK	398	10	0.0260	4473
PSM	KAENIKKF	66	8		4474
PSM	KAENIKKFLY	66	10		4475
PSM	KAFLDELK	59	8		4476
PSM	KAFLDELKA	59	9		4477
PSM	KAWGEVKR	723	8		4478
PSM	KAWGEVKRQIY	723	11		4479
PAP	KDFIATLGK	185	9	0.0006	4480
PAP	KFLNESYK	91	8		4481
PAP	KFLNESYKH	91	9		4482

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSM	KFLYNFTQIPH	72	11		4483
PSA	KFMLCAGR	190	8		4484
PSM	KFSERLQDF	645	9		4485
PSM	KFSERLQDFDK	645	11		4486
PSM	KFSGYPLY	545	8		4487
PSM	KFSGYPLYH	545	9		4488
PAP	KFVTLVFR	36	8		4489
PAP	KFVTLVFRH	36	9		4490
PSM	KFYDPMFK	564	8		4491
PSM	KFYDPMFKY	564	9		4492
PSM	KFYDPMFKYH	564	10		4493
PAP	KGEYFVEMY	322	9	0.0002	4494
PAP	KGEYFVEMYY	322	10	0.0057	4495
PAP	KGEYFVEMYYR	322	11		4496
PSM	KGVILYSDPA	223	10		4497
PSM	KINCSGKIVIA	193	11		4498
PSM	KIVIARYGK	199	9	0.0740	4499
PSM	KIVIARYGKVF	199	11		4500
PSM	KIYSISMK	610	8		4501
PSM	KIYSISMKH	610	9	0.1800	4502
PSM	KLGSGNDF	514	8		4503
PSM	KLGSGNDFEVF	514	11		4504
PAP	KLIMYSAH	282	8		4505
PSM	KLLEKMGGSA	304	10		4506
PSA	KLQCVDLH	166	8		4507
PAP	KLSGLHGQDLF	193	11		4508
PAP	KSEEFQKR	173	8		4509
PAP	KSEEFQKRLH	173	10		4510
PSM	KSLYESWTK	491	9	0.4000	4511
PSM	KSLYESWTKK	491	10	0.3200	4512
PSM	KSNPIVLR	655	8		4513
PSM	KSPDEGFEGK	482	10	0.0044	4514
PSA	KSVILLGR	66	8		4515
PSA	KSVILLGRH	66	9	0.0025	4516
PSM	KTYSVSFDSLF	623	11		4517
PSM	KVFRGNKVK	207	9	0.1600	4518
PSM	KVFRGNKVKNA	207	11		4519
PSM	KVKNAQLA	213	8		4520
PSM	KVKNAQLAGA	213	10		4521
PSM	KVKNAQLAGAK	213	11		4522
Kallikrein	KVLGLPTQEPA	137	11		4523
PSA	KVMDLPTQEPA	133	11		4524
PSM	KVPYNVGPGF	324	10		4525
Kallikrein	KVTEFMLCA	191	9		4526
PSA	KVTKFMLCA	187	9		4527
PSA	KVTKFMLCAGR	187	11		4528

Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
Kallikrein	KVVHYRKWIK	245	10	0.0450	4529
PSA	KVVHYRKWIK	241	10	0.0450	4530
PSM	LAGAKGVILY	219	10	0.0004	4531
PSM	LAGGFFLLGF	28	10		4532
PSM	LAGTEQNF	83	8		4533
PSM	LAGTEQNFQLA	83	11		4534
PSM	LAHYDVLLSY	110	10		4535
PSM	LAKQIQSQWK	92	10	0.0031	4536
PSM	LANSIVLPF	587	9		4537
PAP	LARAASLSLGF	8	11		4538
PSM	LCAGALVLA	21	9		4539
Kallikrein	LCAGLWTGGK	197	10		4540
PSA	LCAGRWTGGK	193	10		4541
PSM	LDELKAENIK	62	10		4542
PSM	LDELKAENIKK	62	11		4543
PAP	LDRSVLAK	26	8		4544
PAP	LDRSVLAKELK	26	11		4545
PSM	LDSVELAH	105	8		4546
PSM	LDSVELAHY	105	9		4547
PAP	LDVYNGLLPPY	300	11		4548
PSM	LFASWDAEEF	417	10		4549
Kallikrein	LFEPEDTGQR	80	10		4550
PSM	LFEPPPPGY	143	9		4551
PAP	LFFWLDRSVLA	22	11		4552
PAP	LFGIWSKVY	202	9		4553
PSA	LFHPEDTGQVF	76	11		4554
PAP	LFLLFFWLDR	19	10		4555
PSM	LFSAVKNF	632	8		4556
PAP	LGEYIRKR	81	8		4557
PAP	LGEYIRKRY	81	9	0.0002	4558
PAP	LGEYIRKRYR	81	10	0.0003	4559
PAP	LGEYIRKRYRK	81	11		4560
PSM	LGFLFGWF	35	8		4561
PSM	LGFLFGWFIK	35	10	0.0007	4562
PAP	LGFLFLLF	16	8		4563
PAP	LGFLFLLFF	16	9		4564
PSM	LGGHRDSWVF	374	10		4565
PSM	LGIASGRA	528	8		4566
PSM	LGIASGRAR	528	9	0.0006	4567
PSM	LGIASGRARY	528	10		4568
PAP	LGKLSGLH	191	8		4569
PSM	LGLPDRPF	679	8		4570
PSM	LGLPDRPFY	679	9		4571
PSM	LGLPDRPFYR	679	10		4572
PSM	LGLPDRPFYRH	679	11		4573
Kallikrein	LGLPTQEPA	139	9		4574

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSA	LGRHSLFH	71	8		4575
PSM	LGSGNDFEVF	515	10		4576
PSM	LGSGNDFEVFF	515	11		4577
PSM	LLEKMGGSA	305	9	0.0006	4578
PAP	LLFFWLDR	21	8		4579
PSM	LLGFLFGWF	34	9		4580
PSM	LLGFLFGWFIK	34	11		4581
PSA	LLGRHSLF	70	8		4582
PSA	LLGRHSLFH	70	9		4583
PSM	LLGSTEWA	428	8		4584
PSM	LLHETDSA	4	8		4585
PSM	LLHETDSAVA	4	10	0.0005	4586
Kallikrein	LLKHQSLR	105	8		4587
PSA	LLKNRFLR	101	8		4588
PAP	LLPPYASCH	306	9	0.0010	4589
PSM	LLQERGVA	441	8		4590
PSM	LLQERGVAY	441	9		4591
Kallikrein	LLRLSEPA	123	8		4592
PSA	LLRLSEPA	119	8		4593
Kallikrein	LLRLSEPAK	123	9		4594
PAP	LLSLYGIH	243	8		4595
PAP	LLSLYGIHK	243	9	0.0760	4596
PAP	LLSLYGIHKQK	243	11		4597
Kallikrein	LLSNDMCA	178	8		4598
Kallikrein	LLSNDMCAR	178	9		4599
Kallikrein	LLSNDMCARA	178	10		4600
Kallikrein	LLSNDMCARAY	178	11		4601
PSM	LLSYPNKTH	116	9	0.0006	4602
PAP	LLWQPIPVH	136	9		4603
PAP	LLYLPFRNCPR	153	11		4604
PSM	LMFLERAF	668	8		4605
Kallikrein	LMLLRLSEPA	121	10		4606
PSA	LMLLRLSEPA	117	10		4607
Kallikrein	LMLLRLSEPAK	121	11		4608
PAP	LMSAMTNLA	113	9	0.0005	4609
PAP	LMSAMTNLAA	113	10	0.0005	4610
PSM	LMYSLVHNLTK	469	11		4611
PAP	LSEDQLLY	148	8		4612
PAP	LSEDQLLYLPF	148	11		4613
PAP	LSELSLLSLY	238	10	0.0005	4614
PSA	LSEPAELTDA	122	10		4615
PAP	LSGLHGQDLF	194	10		4616
PAP	LSLGFLFLLF	14	10		4617
PAP	LSLGFLFLLFF	14	11		4618
PAP	LSLLSLYGIH	241	10	0.0003	4619
PAP	LSLLSLYGIHK	241	11		4620

Table XI

Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PAP	LSLYGHIK	244	8		4621
PAP	LSLYGHIKQK	244	10	0.0520	4622
Kallikrein	LSNDMCAR	179	8		4623
Kallikrein	LSNDMCARA	179	9		4624
Kallikrein	LSNDMCARAY	179	10		4625
Kallikrein	LSVGCTGA	10	8		4626
PSA	LSVTWIGA	6	8		4627
PSA	LSVTWIGAA	6	9		4628
PSM	LSYPNKTH	117	8		4629
PSM	LSYPNKTHPNY	117	11		4630
PSA	LTAAHCIR	57	8		4631
PSA	LTAAHCIRNK	57	10	0.1400	4632
Kallikrein	LTAAHCLK	61	8		4633
Kallikrein	LTAAHCLKK	61	9		4634
PAP	LTELYFEK	315	8	0.0014	4635
PAP	LTELYFEKGEY	315	11		4636
PSA	LTLSVTWIGA	4	10		4637
PSA	LTLSVTWIGAA	4	11		4638
PSM	LTPGYPANEY	268	10	0.0005	4639
PSM	LTPGYPANEYA	268	11		4640
PAP	LTQLGMEQH	70	9		4641
PAP	LTQLGMEQHY	70	10	0.0150	4642
PSA	LVASRGRA	37	8		4643
PSM	LVEKEYDPMF	561	10		4644
PSM	LVEKEYDPMFK	561	11		4645
PAP	LVFRHGDR	40	8	0.0003	4646
PSM	LVHNLTKELK	473	10		4647
Kallikrein	LVHPQWVLTA	54	10		4648
PSA	LVHPQWVLTA	50	10		4649
Kallikrein	LVHPQWVLTAA	54	11		4650
PSA	LVHPQWVLTAA	50	11		4651
PSM	LVLAGGFF	26	8		4652
PAP	LVNEILNH	263	8		4653
PAP	LVNEILNHMK	263	10	0.0560	4654
PAP	LVNEILNHMKR	263	11		4655
PSM	LVYVNYAR	174	8		4656
Kallikrein	MCARAYSEK	183	9		4657
PSA	MDLPTQEPA	135	9		4658
PSM	MFKYHLTVA	569	9		4659
Kallikrein	MLCAGLWTGGK	196	11		4660
PSA	MLCAGRWTGGK	192	11		4661
Kallikrein	MLLRLSEPA	122	9		4662
PSA	MLLRLSEPA	118	9		4663
Kallikrein	MLLRLSEPAK	122	10		4664
PSM	MMNDQLMF	663	8		4665
PSM	MMNDQLMFLER	663	11		4666

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PAP	MSAMTNLA	114	8		4667
PAP	MSAMTNLAA	114	9		4668
PAP	MSAMTNLAALF	114	11		4669
Kallikrein	MSLLKHQSLR	103	10		4670
PSA	MSLLKNRF	99	8		4671
PSA	MSLLKNRFLR	99	10	0.0070	4672
PAP	MTNLAALF	117	8		4673
PSM	NADSSIEGNY	451	10		4674
PSM	NAQLAGAK	216	8		4675
PSM	NCSGKIVIA	195	9		4676
PSM	NCSGKIVIAR	195	10		4677
PSM	NCSGKIVIARY	195	11		4678
PSM	NDFEVFFQR	519	9		4679
Kallikrein	NDMCARAY	181	8		4680
Kallikrein	NDMCARAYSEK	181	11		4681
PSM	NDQLMFLER	665	9		4682
PSM	NDQLMFLERA	665	10		4683
PSM	NDQLMFLERAF	665	11		4684
PSA	NDVCAQVH	177	8		4685
PSA	NDVCAQVHPQK	177	11		4686
PSM	NFSTQKVK	336	8		4687
PSM	NFSTQKVKMH	336	10		4688
PSM	NFTEIASK	638	8		4689
PSM	NFTEIASKF	638	9	0.0005	4690
PAP	NFTLPSWA	220	8		4691
PSM	NFTQIPHLA	76	9		4692
PSM	NGAGDPLTPGY	262	11		4693
PAP	NGLLPPYA	304	8		4694
PAP	NGLLPPYASCH	304	11		4695
PSM	NIKKFLYNF	69	9		4696
PSM	NILNLNGA	257	8		4697
PSM	NITPKHNMK	51	9		4698
PSM	NITPKHNMKA	51	10		4699
PSM	NITPKHNMKAF	51	11		4700
Kallikrein	NLFEPEDTGQR	79	11		4701
PSM	NLLHETDSA	3	9	0.0006	4702
PSM	NLLHETDSAVA	3	11		4703
PSM	NLPGGGVQR	247	9		4704
PSM	NMKAFLDELK	57	10		4705
PSM	NMKAFLDELKA	57	11		4706
Kallikrein	NMSLLKHQSLR	102	11		4707
PSM	NSIVLPFDCR	589	10		4708
Kallikrein	NSQVWLGR	70	8		4709
Kallikrein	NSQVWLGRH	70	9		4710
PSM	NSRLLQER	438	8		4711
PSM	NSRLLQERGVA	438	11		4712

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSM	NVGPGFTGNF	328	10		4713
PSM	NVIGTLRGA	357	9		4714
PSM	NVSDIVPPF	153	9		4715
PSM	NVSDIVPPFSA	153	11		4716
PSM	PADYFAPGVK	231	10		4717
PSA	PAELTDAVK	125	9	0.0002	4718
Kallikrein	PAKITDVVK	129	9		4719
Kallikrein	PALGTTCY	146	8		4720
PSA	PALGTTCY	142	8		4721
Kallikrein	PALGTTCYA	146	9		4722
PSA	PALGTTCYA	142	9		4723
PSM	PANEYAYR	273	8		4724
PSM	PANEYAYRR	273	9	0.0001	4725
Kallikrein	PAVYTKVVH	240	9		4726
Kallikrein	PAVYTKVVHY	240	10		4727
Kallikrein	PAVYTKVVHYR	240	11		4728
Kallikrein	PCALPEKPA	233	9		4729
Kallikrein	PCALPEKPAVY	233	11		4730
PSA	PCALPERPSLY	229	11		4731
PSM	PDEGFEGK	484	8		4732
PSM	PDEGFEGKSLY	484	11		4733
PSM	PDRPFYRH	682	8		4734
PSM	PDRPFYRHVIY	682	11		4735
PSM	PDRYVILGGH	368	10		4736
PSM	PDRYVILGGHR	368	11		4737
PSM	PDSSWRGSLK	315	10		4738
PSM	PFDCRDYA	594	8		4739
PAP	PFRNCPRF	157	8		4740
PSM	PFYRHVIY	685	8		4741
PSM	PFYRHVIYA	685	9		4742
PAP	PGCSPSCPLER	345	11		4743
PSM	PGFTGNFSTQK	331	11		4744
PSM	PGIYDALF	706	8		4745
PSM	PGYPANEY	270	8		4746
PSM	PGYPANEYA	270	9		4747
PSM	PGYPANEYAY	270	10		4748
PSM	PGYPANEYAYR	270	11		4749
PAP	PIDTFPTDPIK	49	11		4750
PSM	PIGYYDAQK	296	9		4751
PAP	PIKESSWPQGF	57	11		4752
PAP	PILLWQPIPVH	134	11		4753
PSM	PLGLPDRPF	678	9		4754
PSM	PLGLPDRPFY	678	10		4755
PSM	PLGLPDRPFYR	678	11		4756
PAP	PLLLARAA	5	8		4757
PSM	PLMYSLVH	468	8		4758

Table XVI

Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PAP	PLSEDQLLY	147	9	0.0005	4759
PSM	PLTPGYPA	267	8		4760
PSM	PLTPGYPANEY	267	11		4761
PAP	PLYCESVH	212	8		4762
PAP	PLYCESVHNF	212	10		4763
PSA	PLYDMSLLK	95	9	0.2400	4764
PSA	PLYDMSLLKNR	95	11		4765
PSM	PLYHSVYETY	550	10	0.0004	4766
Kallikrein	PLYNMSLLK	99	9		4767
Kallikrein	PLYNMSLLKH	99	10		4768
PSM	PMFKYHLTVA	568	10	0.0005	4769
PAP	PSCPLERF	349	8		4770
PAP	PSCPLERFA	349	9		4771
PSM	PSIPVHPIGY	290	10		4772
PSM	PSIPVHPIGYY	290	11		4773
PSM	PSKAWGEVK	721	9		4774
PSM	PSKAWGEVKR	721	10	0.0003	4775
PSA	PSLYTKVVH	236	9		4776
PSA	PSLYTKVVHY	236	10	0.0079	4777
PSA	PSLYTKVVHYR	236	11		4778
PSM	PSPEESGMPR	502	10		4779
PSM	PSSHNKYA	694	8		4780
PAP	PSWATEDTMTK	224	11		4781
PAP	PSYKKLIMY	278	9	0.0002	4782
PAP	PSYKKLIMYSA	278	11		4783
PSM	PVHPIGYY	293	8		4784
PSM	PVHPIGYYDA	293	10		4785
Kallikrein	PVSHSFPH	91	8		4786
Kallikrein	PVSHSFPHPLY	91	11		4787
PSM	QAAAETLSEVA	740	11		4788
PAP	QDLFGIWSK	200	9	0.0006	4789
PAP	QDLFGIWSKVY	200	11		4790
PSM	QGMPEGDLVY	167	10		4791
PAP	QIPSYKKLIMY	276	11		4792
PSM	QIQSQWKEF	95	9		4793
PSM	QIYVAAFTVQA	731	11		4794
PSM	QLAGAKGVILY	218	11		4795
PSM	QLAKQIQSQWK	91	11		4796
PAP	QLGMEQHY	72	8		4797
PAP	QLLYLPFR	152	8		4798
PSM	QLMFLERA	667	8		4799
PSM	QLMFLERAF	667	9		4800
PAP	QLTQLGMEQH	69	10		4801
PAP	QLTQLGMEQHY	69	11		4802
PSM	QSGAAVVH	389	8		4803
Kallikrein	QSLRPDEDSSH	109	11		4804

Table XVI

Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
Kallikrein	QVAVYSHGWA	39	10		4805
Kallikrein	QVAVYSHGWAH	39	11		4806
PSA	QVFQVSHSF	84	9		4807
PSA	QVFQVSHSFPH	84	11		4808
PSA	QVHPQKVTK	182	9	0.0060	4809
PSA	QVHPQKVTKF	182	10		4810
PSA	QVLVASRGR	35	9	0.0021	4811
PSA	QVLVASRGRA	35	10		4812
PSM	QVRGGMVF	578	8		4813
PSM	QVRGGMVFELA	578	11		4814
PSA	QVSHSFPH	87	8		4815
PSA	QVSHSFPHPLY	87	11		4816
Kallikrein	QVWLGRHNLF	72	10		4817
PAP	QVYIRSTDVDR	101	11		4818
PAP	RAAPLLLA	2	8		4819
PAP	RAAPLLLAR	2	9	0.1500	4820
PAP	RAAPLLLARA	2	10		4821
PAP	RAAPLLLARAA	2	11		4822
PAP	RAASLSLGF	10	9		4823
PAP	RAASLSLGFLF	10	11		4824
PAP	RATQIPSY	273	8		4825
PAP	RATQIPSYK	273	9	0.0210	4826
PAP	RATQIPSYKK	273	10	0.0053	4827
PSA	RAVCGGVLVH	43	10	0.0110	4828
Kallikrein	RAYSEKVTEF	186	10		4829
PSM	RDMKINCSGK	190	10	0.0021	4830
PSM	RDYAVVLR	598	8		4831
PSM	RDYAVVLRK	598	9	0.0024	4832
PSM	RDYAVVLRKY	598	10		4833
PSM	RDYAVVLRKYA	598	11		4834
PSA	RFLRPGDDSSH	105	11		4835
PAP	RFQELESETLK	163	11		4836
PSM	RGAVEPDR	363	8		4837
PSM	RGAVEPDRY	363	9		4838
PSM	RGGMVFELA	580	9		4839
PSM	RGNILNLNGA	255	10		4840
PSM	RGNKVKNA	210	8		4841
PSM	RGNKVKNAQLA	210	11		4842
PSM	RGSLKVPY	320	8		4843
PSM	RGVAYINA	445	8		4844
PSM	RISKLGSGNDF	511	11		4845
Kallikrein	RIVGGWECEK	24	10	0.0460	4846
PSA	RIVGGWECEK	20	10	0.0460	4847
Kallikrein	RIVGGWECEKH	24	11		4848
PSA	RIVGGWECEKH	20	11		4849
PSM	RIYNVIGTLR	354	10	0.3700	4850

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSM	RLGIASGR	527	8		4851
PSM	RLGIASGRA	527	9	0.0032	4852
PSM	RLGIASGRAR	527	10		4853
PSM	RLGIASGRARY	527	11		4854
PAP	RLHPYKDF	180	8		4855
PAP	RLHPYKDFIA	180	10	0.0005	4856
PSM	RLLQERGVA	440	9	0.0012	4857
PSM	RLLQERGVAY	440	10	0.0220	4858
PSA	RLSEPAELTDA	121	11		4859
PSM	RMMNDQLMF	662	9		4860
PSM	RSFGTLKK	400	8		4861
Kallikrein	RSLQCVSLH	169	9		4862
PAP	RSVLAKELK	28	9	0.0490	4863
PAP	RSVLAKELKF	28	10		4864
PSM	RTEDFFKLER	181	10		4865
PSM	RTILFASWDA	414	10		4866
PAP	RTLMSAMTNLA	111	11		4867
PSM	RVDCTPLMY	463	9		4868
Kallikrein	RVPVSHSF	89	8		4869
Kallikrein	RVPVSHSFPH	89	10		4870
PAP	SAMTNLAA	115	8		4871
PAP	SAMTNLAALF	115	10		4872
PSM	SAPPDSSWR	312	9	0.0006	4873
PSM	SAVATARR	10	8		4874
PSM	SAVATARRPR	10	10		4875
PSM	SAVKNFTEIA	634	10		4876
PAP	SCHLTELY	312	8		4877
PAP	SCHLTELYF	312	9		4878
PAP	SCHLTELYFEK	312	11		4879
PAP	SCPLERFA	350	8		4880
PSM	SDIVPPFSA	155	9		4881
PSM	SDIVPPFSAF	155	10		4882
PSM	SDPADYFA	229	8		4883
PSM	SFDSLFSA	628	8		4884
PSM	SFDSLFSAVK	628	10		4885
PSM	SFGTLKKEGWR	401	11		4886
PSM	SFPGIYDA	704	8		4887
PSM	SFPGIYDALF	704	10		4888
PSM	SGAAVVHEIVR	390	11		4889
PSM	SGKIVIAR	197	8		4890
PSM	SGKIVIARY	197	9		4891
PSM	SGKIVIARYGK	197	11		4892
PAP	SGLHGQDLF	195	9		4893
PAP	SGLQMALDVY	294	10		4894
PSM	SGMPRISK	507	8		4895
PSM	SGNDFEVF	517	8		4896

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSM	SGNDFEVFF	517	9		4897
PSM	SGNDFEVFFQR	517	11		4898
PSM	SGRARYTK	532	8		4899
Kallikrein	SGWGSIEPEEF	155	11		4900
PSA	SGWGSIEPEEF	151	11		4901
PSM	SGYPLYIISVY	547	10		4902
Kallikrein	SIALSVGCTGA	7	11		4903
PSM	SIEGNYTLR	455	9		4904
Kallikrein	SIEPEEFLR	159	9		4905
Kallikrein	SIEPEEFLRPR	159	11		4906
PSA	SIEPEEFLTPK	155	11		4907
PSM	SIINEDGNEIF	129	11		4908
PSM	SIPVIIPIGY	291	9		4909
PSM	SIPVIIPIGYY	291	10	0.0940	4910
PSM	SISMKIIPQEMK	613	11		4911
PSM	SIVLPFDCR	590	9	0.0006	4912
PSM	SIVLPFDCRDY	590	11		4913
PSM	SLFEPPPPGY	142	10		4914
PSM	SLFSAVKNF	631	9		4915
PAP	SLGFLFLLF	15	9		4916
PAP	SLGFLFLLFF	15	10		4917
Kallikrein	SLIHLLSNDMCA	175	11		4918
Kallikrein	SLLKIIQSLR	104	9		4919
PSA	SLLKNRFLR	100	9	0.0024	4920
PAP	SLLSLYGHI	242	9	0.0006	4921
PAP	SLLSLYGHIK	242	10	0.4900	4922
Kallikrein	SLQCVSLH	170	8		4923
Kallikrein	SLRPDEDSSH	110	10		4924
PAP	SLSLGFLF	13	8		4925
PAP	SLSLGFLFLLF	13	11		4926
PSM	SLVHNLTK	472	8		4927
PSM	SLVHNLTKELK	472	11		4928
PSM	SLYESWTK	492	8		4929
PSM	SLYESWTKK	492	9	1.0000	4930
PAP	SLYGIIKQK	245	9	1.1000	4931
PAP	SLYGIIKQKEK	245	11		4932
PSA	SLYTKVVH	237	8		4933
PSA	SLYTKVVHY	237	9	0.6800	4934
PSA	SLYTKVVHYR	237	10	0.2800	4935
PSA	SLYTKVVHYRK	237	11		4936
PSM	SMKHPQEMK	615	9	0.1100	4937
PSM	SMKHPQEMKTY	615	11		4938
Kallikrein	SSHDLMLLR	117	9	0.0039	4939
PSA	SSHDLMLLR	113	9	0.0039	4940
PSM	SSHNKYAGESF	695	11		4941
PSM	SSIEGNYTLR	454	10	0.0007	4942

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Prostate A03-Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSM	SSNEATNITPK	45	11		4943
PSM	SSWRGSLK	317	8		4944
PSM	SSWRGSLKVPY	317	11		4945
PAP	STDVDRTLMSA	106	11		4946
PAP	STECMTTNSH	369	10		4947
PSM	STEWAEENSR	431	10	0.0005	4948
PSM	STNEVTRIY	348	9	0.0016	4949
PSM	STQKVKMH	338	8		4950
PSM	STQKVKMHHH	338	10		4951
PAP	SVHNFTLPSWA	217	11		4952
PSA	SVILLGRH	67	8		4953
PSA	SVILLGRHSLF	67	11		4954
PAP	SVLAKELK	29	8	0.0017	4955
PAP	SVLAKELKF	29	9		4956
PSM	SVSFDSLF	626	8		4957
PSM	SVSFDSLFSA	626	10		4958
PSA	SVTWIGAA	7	8		4959
PSM	SVYETYELVEK	554	11		4960
PSA	TAAHCIRNK	58	9	0.0094	4961
Kallikrein	TAAHCLKK	62	8		4962
PSM	TARRPRWLCA	14	10		4963
PSM	TDSAVATA	8	8		4964
PSM	TDSAVATAR	8	9		4965
PSM	TDSAVATARR	8	10		4966
PAP	TDVDRTLMSA	107	10		4967
PAP	TFPTDPIK	52	8		4968
Kallikrein	TGAVPLIQSR	15	10		4969
PSM	TGNFSTQK	334	8		4970
PSM	TGNFSTQKVK	334	10	0.0007	4971
Kallikrein	TGQRVPVSH	86	9		4972
Kallikrein	TGQRVPVSHSF	86	11		4973
PSA	TGQVFQVSH	82	9	0.0002	4974
PSA	TGQVFQVSHSF	82	11		4975
PSM	TILFASWDA	415	9		4976
PAP	TLGKLSGLH	190	9		4977
PSM	TLKKEGWR	404	8		4978
PSM	TLKKEGWRPR	404	10	0.0007	4979
PSM	TLKKEGWRPRR	404	11		4980
PAP	TLKSEEFQK	171	9	0.0006	4981
PAP	TLKSEEFQKR	171	10	0.0007	4982
PAP	TLMSAMTNLA	112	10	0.0005	4983
PAP	TLMSAMTNLAA	112	11		4984
PSM	TLRGAVEPDR	361	10	0.0003	4985
PSM	TLRGAVEPDRY	361	11		4986
PSM	TLRVDCTPLMY	461	11		4987
PSA	TLSVTWIGA	5	9		4988

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSA	TLSVTWIGAA	5	10		4989
PAP	TLVFRHGDR	39	9	0.0006	4990
PSM	TSLFEPPPPGY	141	11		4991
Kallikrein	TSWGPEPCA	227	9		4992
PSA	TSWGSEPCA	223	9		4993
PAP	TTVSGLQMA	291	9		4994
PSM	TVAQVRGGMVF	575	11		4995
PAP	TVPLSEDQLLY	145	11		4996
PAP	TVSGLQMA	292	8		4997
PSM	VAAFTVQA	734	8		4998
PSM	VAAFTVQAA	734	9		4999
PSM	VAAFTVQAAA	734	10		5000
PSM	VAQVRGGMVF	576	10		5001
PSM	VATARRPR	12	8		5002
Kallikrein	VAVYSHGWA	40	9		5003
Kallikrein	VAVYSHGWAH	40	10		5004
PSA	VCAQVHPQK	179	9		5005
PSA	VCGGVLVH	45	8		5006
PSM	VDCTPLMY	464	8		5007
PSM	VDPSKAWGEVK	719	11		5008
PAP	VDRTLMSA	109	8		5009
PSM	VFFQRLGIA	523	9		5010
PSM	VFGGIDPQSGA	382	11		5011
PSA	VFQVSHSF	85	8		5012
PSA	VFQVSHSFPH	85	10		5013
PSM	VFRGNKVK	208	8		5014
PSM	VFRGNKVKNA	208	10		5015
Kallikrein	VGGWECEK	26	8		5016
PSA	VGGWECEK	22	8		5017
Kallikrein	VGGWECEKH	26	9		5018
PSA	VGGWECEKH	22	9		5019
PSM	VGLPSIPVH	287	9		5020
PSM	VGPGFTGNF	329	9		5021
PSM	VIARYGKVF	201	9		5022
PSM	VIARYGKVFR	201	10		5023
PSM	VIGTLRGA	358	8		5024
PSA	VILLGRHSLF	68	10		5025
PSA	VILLGRHSLFH	68	11		5026
PSM	VILYSDPA	225	8		5027
PSM	VILYSDPADY	225	10		5028
PSM	VILYSDPADYF	225	11		5029
PSA	VISNDVCA	174	8		5030
PSA	VISNDVCAQVH	174	11		5031
PSM	VIYAPSSH	690	8		5032
PSM	VIYAPSSHNK	690	10	0.5400	5033
PSM	VIYAPSSHNKY	690	11		5034

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Prostate A03* Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSM	VLAGGFFLLGF	27	11		5035
PAP	VLAKELKF	30	8		5036
Kallikrein	VLGLPTQEPA	138	10		5037
PSM	VLLSYPNK	115	8		5038
PSM	VLLSYPNKTH	115	10		5039
PSM	VLPFDCRDY	592	9		5040
PSM	VLPFDCRDYA	592	10	0.0005	5041
PSM	VLRKYADK	603	8		5042
PSM	VLRKYADKIY	603	10		5043
PSM	VLRMMNDQLMF	660	11		5044
PSA	VLTAAHCIR	56	9	0.0002	5045
PSA	VLTAAHCIRNK	56	11		5046
Kallikrein	VLTAAHCLK	60	9		5047
Kallikrein	VLTAAHCLKK	60	10		5048
PSA	VLVASRGR	36	8		5049
PSA	VLVASRGRA	36	9		5050
Kallikrein	VLVHPQWVLTA	53	11		5051
PSA	VLVHPQWVLTA	49	11		5052
PAP	VLVNELNH	262	9	0.0019	5053
PAP	VLVNELNHMK	262	11		5054
PSA	VMDLPTQEPA	134	10		5055
PSM	VSDIVPPF	154	8		5056
PSM	VSDIVPPFSA	154	10		5057
PSM	VSDIVPPFSAF	154	11		5058
PSM	VSFDSLFSA	627	9		5059
PSM	VSFDSLFSAVK	627	11		5060
PAP	VSGLQMALDVY	293	11		5061
Kallikrein	VSHSFPHPLY	92	10	0.0003	5062
PSA	VSHSFPHPLY	88	10	0.0003	5063
Kallikrein	VTEFMLCA	192	8		5064
PSA	VTKFMLCA	188	8		5065
PSA	VTKFMLCAGR	188	10	0.0003	5066
PAP	VTLVFRHGDR	38	10		5067
PSM	VVHEIVRSF	394	9		5068
Kallikrein	VVHYRKWIK	246	9	0.0072	5069
PSA	VVHYRKWIK	242	9	0.0072	5070
PSM	VVLRKYADK	602	9	0.0390	5071
PSM	VVLRKYADKIY	602	11		5072
Kallikrein	WAHCGGVLVH	47	10		5073
PAP	WATEDTMTK	226	9	0.0006	5074
PAP	WATEDTMTKLR	226	11		5075
Kallikrein	WDLVLSIA	2	8		5076
PSM	WFIKSSNEA	41	9		5077
PSM	WGEVKRQIY	725	9		5078
PSM	WGEVKRQIYVA	725	11		5079
Kallikrein	WGPEPCALPEK	229	11		5080

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Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PSA	WGSEPCALPER	225	11		5081
Kallikrein	WGSIEPEEF	157	9		5082
PSA	WGSIEPEEF	153	9		5083
Kallikrein	WGSIEPEEFLR	157	11		5084
PSA	WIGAAPLILSR	10	11		5085
Kallikrein	WIKDTIAA	252	8		5086
PSA	WIKDTIVA	248	8		5087
PSM	WLCAGALVLA	20	10	0.0026	5088
PAP	WLDRSVLA	25	8		5089
PAP	WLDRSVLAK	25	9	0.0035	5090
Kallikrein	WLGRIHNLF	74	8		5091
PAP	WSKVYDPLY	206	9	0.0002	5092
PAP	WSTECMTTNSH	368	11		5093
PSM	WTKKSPSPEF	497	10		5094
PSA	WVLTAAHCIR	55	10	0.0004	5095
Kallikrein	WVLTAAHCLK	59	10		5096
Kallikrein	WVLTAAHCLKK	59	11		5097
PSM	YADKIYSISMK	607	11		5098
PSM	YAGESFPGIY	700	10		5099
PSM	YAPSSHNK	692	8		5100
PSM	YAPSSHNKY	692	9		5101
PSM	YAPSSHNKYA	692	10		5102
PSM	YARTEDFF	179	8		5103
PSM	YARTEDFFK	179	9		5104
PAP	YASCHLTELY	310	10	0.0003	5105
PAP	YASCHLTELYF	310	11		5106
PSM	YAVVLRKY	600	8		5107
PSM	YAVVLRKYA	600	9		5108
PSM	YAVVLRKYADK	600	11		5109
PSM	YAYRRGIA	277	8		5110
PSM	YAYRRGIAEA	277	10		5111
PAP	YCESVHNF	214	8		5112
PSM	YDALFDIESK	709	10		5113
PSM	YDAQKLLEK	300	9	0.0006	5114
PSA	YDMSLLKNR	97	9		5115
PSA	YDMSLLKNRF	97	10		5116
PAP	YDPLYCESVH	210	10		5117
PSM	YDPMFKYH	566	8		5118
PSM	YDVLLSYPNK	113	10	0.0005	5119
PSM	YFAPGVKSY	234	9		5120
PAP	YFEKGEYF	319	8		5121
PAP	YFVEMYYR	325	8		5122
PAP	YGHHKQKEK	247	9	0.0006	5123
PAP	YGHHKQKEKSR	247	11		5124
PSM	YGKVFRGNK	205	9	0.0006	5125
PSM	YGKVFRGNKVK	205	11		5126

Table XVI

Prostate A03 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*0301	Seq. Id. No.
PAP	YIRKRYRK	84	8		5127
PAP	YIRKRYRKF	84	9		5128
PAP	YIRSTDVDR	103	9		5129
PAP	YLPFRNCPR	155	9		5130
PAP	YLPFRNCPRF	155	10		5131
PSM	YSDPADYF	228	8		5132
PSM	YSDPADYFA	228	9		5133
Kallikrein	YSEKVTEF	188	8		5134
PSM	YSLVHNLTK	471	9	0.0600	5135
PSM	YSVSFDSLF	625	9		5136
PSM	YSVSFDSLFSA	625	11		5137
PSM	YTKNWETNK	537	9		5138
PSM	YTKNWETNKF	537	10		5139
Kallikrein	YTKVVHYR	243	8		5140
PSA	YTKVVHYR	239	8		5141
Kallikrein	YTKVVHYRK	243	9	0.0006	5142
PSA	YTKVVHYRK	239	9	0.0006	5143
PSM	YVAAFTVQA	733	9		5144
PSM	YVAAFTVQAA	733	10		5145
PSM	YVAAFTVQAAA	733	11		5146
PSM	YVILGGHR	371	8		5147
PSM	YVNYARTEDF	176	10		5148
PSM	YVNYARTEDFF	176	11		5149

Table XVII

Prostate A*1101 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PSA	AAHCIRNK	59	8		5150
PSA	AAPLILSR	13	8		5151
PAP	AAPLLLAR	3	8		5152
PSM	AAVVHEIVR	392	9		5153
PSM	ADKIYSISMK	608	10		5154
PSM	ADKIYSISMKH	608	11		5155
PSM	ADSSIEGNY	452	9		5156
PSM	ADYFAPGVK	232	9	0.0051	5157
PSM	ADYFAPGVKSY	232	11		5158
PSM	AFIDPLGLPDR	674	11		5159
PSM	AGAKGVILY	220	9		5160
PSM	AGDPLTPGY	264	9		5161
PSM	AGESFPGIY	701	9		5162
Kallikrein	AGLWTGGK	199	8		5163
PSA	AGRWTGGK	195	8		5164
PSM	AGTEQNFQLAK	84	11		5165
PSM	ALFDIESK	711	8		5166
Kallikrein	ALPEKPAVY	235	9		5167
Kallikrein	ALPEKPAVYTK	235	11		5168
PSA	ALPERPSLY	231	9	0.0013	5169
PSA	ALPERPSLYTK	231	11		5170
PSM	ANEYAYRR	274	8		5171
PSM	ANSIVLPFDCR	588	11		5172
PAP	ASCHLTELY	311	9	0.0550	5173
PSM	ASGRARYTK	531	9	0.2700	5174
PAP	ATEDTMTK	227	8	0.0039	5175
PAP	ATEDTMTKLR	227	10		5176
PAP	ATLGKLSGLH	189	10		5177
PSM	ATNITPKH	49	8		5178
PSM	ATNITPKHNMK	49	11		5179
PAP	ATQIPSYK	274	8	0.0700	5180
PAP	ATQIPSYKK	274	9	1.2000	5181
PSM	AVATARRPR	11	9		5182
PSA	AVCGGVLVH	44	9		5183
PSM	AVGLPSIPVH	286	10		5184
PSM	AVKNFTEIASK	635	11		5185
Kallikrein	AVPLIQSR	17	8		5186
PSM	AVVHEIVR	393	8		5187
PSM	AVVLRKYADK	601	10	0.0210	5188
Kallikrein	AVYSHGWAH	41	9		5189
Kallikrein	AVYTKVVH	241	8		5190
Kallikrein	AVYTKVVHY	241	9		5191
Kallikrein	AVYTKVVHYR	241	10		5192
Kallikrein	AVYTKVVHYRK	241	11		5193
Kallikrein	CAGLWTGGK	198	9		5194
PSA	CAGRWTGGK	194	9	0.0015	5195

Table XVII

Prostate All Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
Kallikrein	CALPEKPAVY	234	10		5196
PSA	CALPERPSLY	230	10		5197
PSA	CAQVHPQK	180	8		5198
PSA	CAQVHPQKVTK	180	11		5199
Kallikrein	CARAYSEK	184	8		5200
PSM	CSGKIVIAR	196	9		5201
PSM	CSGKIVIARY	196	10	0.0490	5202
PAP	CSPSCPLER	347	9	0.0006	5203
Kallikrein	CTGAVPLIQSR	14	11		5204
PSM	CTPLMYSLVH	466	10		5205
PSM	DALFDIESK	710	9	0.0002	5206
PSM	DAQKLLEK	301	8		5207
PSM	DCRDYAVVLR	596	10		5208
PSM	DCRDYAVVLRK	596	11		5209
PSM	DCTPLMYSLVH	465	11		5210
PSA	DDSSHDLMLLR	111	11		5211
PSM	DFDKSNPIVLR	652	11		5212
PSM	DFEVFFQR	520	8		5213
PSM	DFFKLERDMK	184	10		5214
PAP	DFIATLGK	186	8		5215
PSM	DIESKVDPSK	714	10	0.0002	5216
PAP	DLFGIWSK	201	8		5217
PAP	DLFGIWSKVY	201	10		5218
PSM	DLVYVNYAR	173	9		5219
Kallikrein	DMCARAYSEK	182	10		5220
PSM	DMKINCSGK	191	9		5221
PSA	DMSLLKNR	98	8	0.0001	5222
PSA	DMSLLKNRFLR	98	11		5223
PSM	DSAVATAR	9	8		5224
PSM	DSAVATARR	9	9		5225
PSM	DSAVATARRPR	9	11		5226
PSM	DSLFSAVK	630	8		5227
Kallikrein	DSSHDLMLLR	116	10		5228
PSA	DSSHDLMLLR	112	10		5229
PSM	DSSIEGNY	453	8		5230
PSM	DSSIEGNYTLR	453	11		5231
PSM	DSSWRGSLK	316	9	0.0003	5232
PSM	DSVELAHY	106	8		5233
PAP	DTFPTDPIK	51	9	0.0001	5234
Kallikrein	DTGQRVPVSH	85	10		5235
PSA	DTGQVFQVSH	81	10		5236
PSA	DVCAQVHPQK	178	10	0.0011	5237
PSM	DVLLSYPNK	114	9	0.0010	5238
PSM	DVLLSYPNKTH	114	11		5239
PAP	DVYNGLLPPY	301	10		5240
PSM	EATNITPK	48	8		5241

Table XVII

Prostate A11 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PSM	EATNITPKH	48	9		5242
PSM	EAVGLPSIPVH	285	11		5243
PAP	ECMTTNSH	371	8		5244
PSM	EDFFKLER	183	8		5245
PSM	EDFFKLERDMK	183	11		5246
PAP	EDQLLYLPFR	150	10		5247
Kallikrein	EDSSHDLMLLR	115	11		5248
Kallikrein	EDTGQRVPVSH	84	11		5249
PSA	EDTGQVFQVSH	80	11		5250
PAP	EDTMTKLR	229	8		5251
PSM	EFGLDSVELAH	102	11		5252
PAP	EFQKRLHPY	176	9		5253
PAP	EFQKRLHPYK	176	10		5254
PSM	EFSGMPRISK	505	10		5255
PSM	EGDLVYVNY	171	9		5256
PSM	EGDLVYVNYAR	171	11		5257
PSM	EGFEGKSLY	486	9		5258
PSM	EGKSLYESWTK	489	11		5259
PSM	EIASKFSER	641	9	0.0002	5260
PAP	EILNHMKR	266	8		5261
PSM	EIVRSFGTLK	397	10		5262
PSM	EIVRSFGTLKK	397	11		5263
PSM	ELAHYDVLLSY	109	11		5264
PAP	ELESETLK	166	8		5265
PAP	ELGEYIRK	80	8		5266
PAP	ELGEYIRKR	80	9		5267
PAP	ELGEYIRKRY	80	10		5268
PAP	ELGEYIRKRYR	80	11		5269
PSM	ELKAENIK	64	8		5270
PSM	ELKAENIKK	64	9		5271
PAP	ELKFVTLVFR	34	10	0.0037	5272
PAP	ELKFVTLVFRH	34	11		5273
PAP	ELSELSLLSLY	237	11		5274
PAP	ELSLLSLY	240	8		5275
PAP	ELSLLSLYGIH	240	11		5276
PAP	ELYFEKGEY	317	9		5277
PAP	EMYYRNETQH	328	10		5278
PSM	ENIKKFLY	68	8		5279
PSM	ENSRLLQER	437	9		5280
PSM	ESKVDPSK	716	8		5281
PAP	ESYKHEQVY	95	9	0.0002	5282
PAP	ESYKHEQVYIR	95	11		5283
PSM	ETDSAVATAR	7	10		5284
PSM	ETDSAVATARR	7	11		5285
PAP	ETLKSEEFQK	170	10	0.0140	5286
PAP	ETLKSEEFQKR	170	11		5287

Table XVIC

Prostate A11 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PSM	ETNKFSGY	542	8		5288
PSM	ETNKFSGYPLY	542	11		5289
PSM	ETYELVEK	557	8		5290
PSM	ETYELVEKFY	557	10	0.0002	5291
PSM	FAPGVKSY	235	8		5292
PSM	FDCRDYAVVLR	595	11		5293
PSM	FDIESKVDPSK	713	11		5294
PSM	FDKSNPIVLR	653	10		5295
PSM	FDSLFSAVK	629	9		5296
PSM	FFKLERDMK	185	9		5297
PSM	FFQRLGIASGR	524	11		5298
PAP	FFWLDRSVLAK	23	11		5299
PAP	FGIWSKVY	203	8		5300
PSM	FGLDSVELAH	103	10		5301
PSM	FGLDSVELAHY	103	11		5302
PSM	FGTLKKEGWR	402	10		5303
PSM	FIDPLGLPDR	675	10		5304
PSM	FLDELKAENIK	61	11		5305
PSM	FLFGWFIK	37	8		5306
PAP	FLFLLFFWLDR	18	11		5307
PAP	FLLFFWLDR	20	9	0.0004	5308
PAP	FLNESYKH	92	8		5309
PSA	FLRPGDDSSH	106	10		5310
PSM	FLYNFTQIPH	73	10	0.0036	5311
PSM	FSERLQDFDK	646	10	0.0007	5312
PSM	FSGMPRISK	506	9		5313
PSM	FSGYPLYH	546	8		5314
PSM	FSGYPLYHSVY	546	11		5315
PSM	FSTQKVKMH	337	9		5316
PSM	FSTQKVKMHHH	337	11		5317
PSM	FTEIASKFSER	639	11		5318
PSM	FTGNFSTQK	333	9		5319
PSM	FTGNFSTQKVK	333	11		5320
PAP	FVTLVFRH	37	8		5321
PAP	FVTLVFRHGDR	37	11		5322
PSA	GAAPLILSR	12	9	0.0350	5323
PSM	GAAVVHEIVR	391	10		5324
PSM	GAGDPLTPGY	263	10		5325
PSM	GAKGVILY	221	8		5326
PSM	GAVEPDRY	364	8		5327
Kallikrein	GAVPLIQSR	16	9		5328
PAP	GCSPSCPLER	346	10		5329
PSM	GDLVYVNY	172	8		5330
PSM	GDLVYVNYAR	172	10		5331
PSM	GDPLTPGY	265	8		5332
PSM	GFEGKSLY	487	8		5333

Table XVII

Prostate A11 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PSM	GFLFGWFIK	36	9	0.0014	5334
PSM	GFTGNFSTQK	332	10		5335
PSM	GGSAPPDSSWR	310	11		5336
PAP	GGVLVNEILNH	260	11		5337
Kallikrein	GGWECEKH	27	8		5338
PSA	GGWECEKH	23	8		5339
PSM	GIASGRAR	529	8		5340
PSM	GIASGRARY	529	9		5341
PSM	GIASGRARYTK	529	11		5342
PAP	GIHKQKEK	248	8		5343
PAP	GIHKQKEKSR	248	10		5344
PAP	GIWSKVYDPLY	204	11		5345
PSM	GLDSVELAH	104	9		5346
PSM	GLDSVELAHY	104	10		5347
PAP	GLLPPYASCH	305	10		5348
PSM	GLPDRPFY	680	8		5349
PSM	GLPDRPFYR	680	9	0.0280	5350
PSM	GLPDRPFYRH	680	10		5351
PSM	GLPSIPVH	288	8		5352
PAP	GLQMALDVY	295	9		5353
PAP	GMEQHYELGEY	74	11		5354
PSM	GMPEGDLVY	168	9	0.0002	5355
PSM	GNDFEVFFQR	518	10		5356
PSM	GNFSTQKVK	335	9		5357
PSM	GNFSTQKVKMH	335	11		5358
PSM	GSAPPDSSWR	311	10	0.1400	5359
PSA	GSEPCALPER	226	10		5360
Kallikrein	GSHPEEFLR	158	10		5361
PSM	GSTEWAEENSR	430	11		5362
PSM	GTEQNFQLAK	85	10		5363
PSM	GTLKKEGWR	403	9		5364
PSM	GTLKKEGWRPR	403	11		5365
PSM	GTLRGAVEPDR	360	11		5366
PSM	GVILYSDPADY	224	11		5367
PAP	GVLVNEILNH	261	10		5368
Kallikrein	HCGGVLVH	49	8		5369
PAP	HGQDLFGIWSK	198	11		5370
PSM	HIHSTNEVTR	345	10		5371
Kallikrein	HLLSNDMCAR	177	10		5372
PAP	HLTELYFEK	314	9	0.5300	5373
PSM	HLTVAQVR	573	8		5374
PAP	HMKRATQIPSY	270	11		5375
PSM	HNLTKELK	475	8		5376
PSM	HNMKAFLDELK	56	11		5377
Kallikrein	HSFPHPLY	94	8	0.0006	5378
PSA	HSFPHPLY	90	8	0.0006	5379

Table XVII

Prostate A*1101 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
Kallikrein	HSQPWQVAVY	34	10		5380
PSM	HSTNEVTR	347	8		5381
PSM	HSTNEVTRIY	347	10	0.0002	5382
PSM	HVIYAPSSH	689	9		5383
PSM	HVIYAPSSHNK	689	11		5384
PSM	IARYGKVFR	202	9		5385
PSM	IASGRARY	530	8		5386
PSM	IASGRARYTK	530	10		5387
PSM	IASKFSER	642	8		5388
PAP	IATLGKLSGLH	188	11		5389
PSM	IDPLGLPDR	676	9		5390
PSM	IDPQSGAAVVH	386	11		5391
PAP	IDTFPTDPIK	50	10		5392
PSA	IGAAPLILSR	11	10		5393
PSM	IGYYDAQK	297	8		5394
PSA	ILLGRHSLFH	69	10		5395
PAP	ILLWQPIPVH	135	10		5396
PSM	ILYSDPADY	226	9		5397
PSM	INADSSIEGNY	450	11		5398
PSM	INCSGKIVIAR	194	11		5399
PSM	ISMKHPQEMK	614	10	0.1100	5400
PSA	ISNDVCAQVH	175	10		5401
PSM	ITPKHNMK	52	8		5402
Kallikrein	IVGGWECEK	25	9	0.0190	5403
PSA	IVGGWECEK	21	9	0.0190	5404
Kallikrein	IVGGWECEKH	25	10		5405
PSA	IVGGWECEKH	21	10		5406
PSM	IVIARYGK	200	8		5407
PSM	IVIARYGKVFR	200	11		5408
PSM	IVLPFDCR	591	8		5409
PSM	IVLPFDCRDY	591	10		5410
PSM	IVRSFGTLK	398	9	0.0087	5411
PSM	IVRSFGTLKK	398	10	0.0006	5412
PSM	KAENIKKFLY	66	10		5413
PSM	KAFLDELK	59	8		5414
PSM	KAWGEVKR	723	8		5415
PSM	KAWGEVKRQIY	723	11		5416
PAP	KDFIATLGK	185	9	0.0004	5417
PAP	KFLNESYK	91	8		5418
PAP	KFLNESYKH	91	9		5419
PSM	KFLYNFTQIPH	72	11		5420
PSA	KFMLCAGR	190	8		5421
PSM	KFSERLQDFDK	645	11		5422
PSM	KFSGYPLY	545	8		5423
PSM	KFSGYPLYH	545	9		5424
PAP	KFVTLVFR	36	8		5425

Table XVII

Prostate A11 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PAP	KFVTLVFRH	36	9		5426
PSM	KFYDPMFK	564	8		5427
PSM	KFYDPMFKY	564	9		5428
PSM	KFYDPMFKYH	564	10		5429
PAP	KGEYFVEMY	322	9	0.0002	5430
PAP	KGEYFVEMYY	322	10	0.0890	5431
PAP	KGEYFVEMYYR	322	11		5432
PSM	KIVIARYGK	199	9	1.0000	5433
PSM	KIYSISMK	610	8		5434
PSM	KIYSISMKH	610	9	0.1200	5435
PAP	KLIMYSAH	282	8		5436
PSA	KLQCVDLH	166	8		5437
PSM	KNAQLAGAK	215	9		5438
PSM	KNFTEIASK	637	9		5439
Kallikrein	KNSQVWLGR	69	9		5440
Kallikrein	KNSQVWLGRH	69	10		5441
PSM	KNWETNKFSGY	539	11		5442
PAP	KSEEFQKR	173	8		5443
PAP	KSEEFQKRLH	173	10		5444
PSM	KSLYESWTK	491	9	2.1000	5445
PSM	KSLYESWTKK	491	10	0.0810	5446
PSM	KSNPIVLR	655	8		5447
PSM	KSPDEGFEGK	482	10	0.0210	5448
PSA	KSVILLGR	66	8		5449
PSA	KSVILLGRH	66	9	0.0014	5450
PSM	KVFRGNKVK	207	9	0.1200	5451
PSM	KVKNAQLAGAK	213	11		5452
PSA	KVTKFMLCAGR	187	11		5453
Kallikrein	KVVHYRKWIK	245	10	0.0450	5454
PSA	KVVHYRKWIK	241	10	0.0450	5455
PSM	LAGAKGVILY	219	10	0.0002	5456
PSM	LAHYDVLLSY	110	10		5457
PSM	LAKQIQSQWK	92	10	0.0007	5458
Kallikrein	LCAGLWTGGK	197	10		5459
PSA	LCAGRWTGGK	193	10		5460
PSM	LDELKAENIK	62	10		5461
PSM	LDELKAENIKK	62	11		5462
PAP	LDRSVLAK	26	8		5463
PAP	LDRSVLAKELK	26	11		5464
PSM	LDSVELAH	105	8		5465
PSM	LDSVELAHY	105	9		5466
PAP	LDVYNGLLPPY	300	11		5467
Kallikrein	LFEPEDTGQR	80	10		5468
PSM	LFEPPPPGY	143	9		5469
PAP	LFGIWSKVY	202	9		5470
PAP	LFLLFFWLDR	19	10		5471

Table XVII

Prostate A*11 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PAP	LGEYIRKR	81	8		5472
PAP	LGEYIRKRY	81	9	0.0002	5473
PAP	LGEYIRKRYR	81	10	0.0002	5474
PAP	LGEYIRKRYRK	81	11		5475
PSM	LGFLFGWFIK	35	10	0.3700	5476
PSM	LGIASGRAR	528	9	0.0002	5477
PSM	LGIASGRARY	528	10		5478
PAP	LGKLSGLH	191	8		5479
PSM	LGLPDRPFY	679	9		5480
PSM	LGLPDRPFYR	679	10		5481
PSM	LGLPDRPFYRH	679	11		5482
PSA	LGRHSLFH	71	8		5483
PAP	LLFFWLDR	21	8		5484
PSM	LLGFLFGWFIK	34	11		5485
PSA	LLGRHSLFH	70	9		5486
Kallikrein	LLKHQSLR	105	8		5487
PSA	LLKNRFLR	101	8		5488
PAP	LLPPYASCH	306	9	0.0002	5489
PSM	LLQERGVAY	441	9		5490
Kallikrein	LLRLSEPAK	123	9		5491
PAP	LLSLYGHH	243	8		5492
PAP	LLSLYGHHK	243	9	0.2000	5493
PAP	LLSLYGHHKQK	243	11		5494
Kallikrein	LLSNDMCAR	178	9		5495
Kallikrein	LLSNDMCARAY	178	11		5496
PSM	LLSYPNKTH	116	9	0.0003	5497
PAP	LLWQPIPVH	136	9		5498
PAP	LLYLPERNCPR	153	11		5499
Kallikrein	LMLLRLSEPAK	121	11		5500
PSM	LMYSLVHNLTK	469	11		5501
PAP	LNESYKHEQVY	93	11		5502
PAP	LSEDQLLY	148	8		5503
PAP	LSELSLLSLY	238	10	0.0004	5504
PAP	LSLLSLYGHH	241	10	0.0002	5505
PAP	LSLLSLYGHHK	241	11		5506
PAP	LSLYGHHK	244	8		5507
PAP	LSLYGHHKQK	244	10	0.0370	5508
Kallikrein	LSNDMCAR	179	8		5509
Kallikrein	LSNDMCARAY	179	10		5510
PSM	LSYPNKTH	117	8		5511
PSM	LSYPNKTHPNY	117	11		5512
PSA	LTAAHCIR	57	8		5513
PSA	LTAAHCIRNK	57	10	0.0830	5514
Kallikrein	LTAAHCLK	61	8		5515
Kallikrein	LTAAHCLKK	61	9		5516
PAP	LTELYFEK	315	8	0.0100	5517

Table XVII

Prostate A1 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PAP	LTELYFEKGEY	315	11		5518
PSM	LTPGYPANEY	268	10	0.0002	5519
PAP	LTQLGMEQH	70	9		5520
PAP	LTQLGMEQHY	70	10	0.0024	5521
PSM	LVEKFYDPMFK	561	11		5522
PAP	LVFRHGDR	40	8	0.0002	5523
PSM	LVHNLTKELK	473	10		5524
PAP	LVNEILNH	263	8		5525
PAP	LVNEILNHMK	263	10	0.1200	5526
PAP	LVNEILNHMKR	263	11		5527
PSM	LVYVNYAR	174	8		5528
Kallikrein	MCARAYSEK	183	9		5529
Kallikrein	MLCAGLWTGGK	196	11		5530
PSA	MLCAGRWTGGK	192	11		5531
Kallikrein	MLLRLSEPAK	122	10		5532
PSM	MMNDQLMFLER	663	11		5533
PSM	MNDQLMFLER	664	10		5534
Kallikrein	MSLLKHQSLR	103	10		5535
PSA	MSLLKNRFLR	99	10	0.0110	5536
PSM	NADSSIEGNY	451	10		5537
PSM	NAQLAGAK	216	8		5538
PSM	NCSGKIVIAR	195	10		5539
PSM	NCSGKIVIARY	195	11		5540
PSM	NDFEVFFQR	519	9		5541
Kallikrein	NDMCARAY	181	8		5542
Kallikrein	NDMCARAYSEK	181	11		5543
PSM	NDQLMFLER	665	9		5544
PSA	NDVCAQVH	177	8		5545
PSA	NDVCAQVHPQK	177	11		5546
PSM	NFSTQKVK	336	8		5547
PSM	NFSTQKVKMH	336	10		5548
PSM	NFTEIASK	638	8		5549
PSM	NGAGDPLTPGY	262	11		5550
PAP	NGLLPPYASCH	304	11		5551
PSM	NITPKHNMK	51	9		5552
Kallikrein	NLFEPEDTGQR	79	11		5553
PSM	NLPGGGVQR	247	9		5554
PSM	NMKAFLDELK	57	10		5555
Kallikrein	NMSLLKHQSLR	102	11		5556
PSM	NSIVLPFDCR	589	10		5557
Kallikrein	NSQVWLGR	70	8		5558
Kallikrein	NSQVWLGRH	70	9		5559
PSM	NSRLLQER	438	8		5560
PSM	PADYFAPGVK	231	10		5561
PSA	PAELTDAVK	125	9	0.0002	5562
Kallikrein	PAKITDVVK	129	9		5563

Table XVII

Prostate A11 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
Kallikrein	PALGTTCY	146	8		5564
PSA	PALGTTCY	142	8		5565
PSM	PANEYAYR	273	8		5566
PSM	PANEYAYRR	273	9	0.0002	5567
Kallikrein	PAVYTKVVH	240	9		5568
Kallikrein	PAVYTKVVHY	240	10		5569
Kallikrein	PAVYTKVVHYR	240	11		5570
Kallikrein	PCALPEKPAVY	233	11		5571
PSA	PCALPERPSLY	229	11		5572
PSM	PDEGFEGK	484	8		5573
PSM	PDEGFEGKSLY	484	11		5574
PSM	PDRPFYRH	682	8		5575
PSM	PDRPFYRHVIY	682	11		5576
PSM	PDRYVILGGH	368	10		5577
PSM	PDRYVILGGHR	368	11		5578
PSM	PDSSWRGSLK	315	10		5579
PSM	PFYRHVIY	685	8		5580
PAP	PGCSPSCPLER	345	11		5581
PSM	PGFTGNFSTQK	331	11		5582
PSM	PGYPANEY	270	8		5583
PSM	PGYPANEYAY	270	10		5584
PSM	PGYPANEYAYR	270	11		5585
PAP	PIDTFPTDPIK	49	11		5586
PSM	PIGYYDAQK	296	9		5587
PAP	PILLWQPIPVH	134	11		5588
PSM	PLGLPDRPFY	678	10		5589
PSM	PLGLPDRPFYR	678	11		5590
PSM	PLMYSLVH	468	8		5591
PAP	PLSEDQLLY	147	9	0.0001	5592
PSM	PLTPGYPANEY	267	11		5593
PAP	PLYCESVH	212	8		5594
PSA	PLYDMSLLK	95	9	0.0370	5595
PSA	PLYDMSLLKNR	95	11		5596
PSM	PLYHSVYETY	550	10	0.0002	5597
Kallikrein	PLYNMSLLK	99	9		5598
Kallikrein	PLYNMSLLKH	99	10		5599
PSM	PNKTHPNY	120	8		5600
PSM	PSIPVHPIGY	290	10		5601
PSM	PSIPVHPIGYY	290	11		5602
PSM	PSKAWGEVK	721	9		5603
PSM	PSKAWGEVKR	721	10	0.0002	5604
PSA	PSLYTKVVH	236	9		5605
PSA	PSLYTKVVHY	236	10	0.0003	5606
PSA	PSLYTKVVHYR	236	11		5607
PSM	PSPEFSGMPR	502	10		5608
PAP	PSWATEDTMTK	224	11		5609

Table XVII

Prostate ALL Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PAP	PSYKKLIMY	278	9	0.0002	5610
PSM	PVHPIGYY	293	8		5611
Kallikrein	PVSHSFPH	91	8		5612
Kallikrein	PVSHSFPHPLY	91	11		5613
PAP	QDLFGIWSK	200	9	0.0008	5614
PAP	QDLFGIWSKVY	200	11		5615
PSM	QGMPEGDLVY	167	10		5616
PAP	QIPSYKKLIMY	276	11		5617
PSM	QLAGAKGVILY	218	11		5618
PSM	QLAKQIQSQWK	91	11		5619
PAP	QLGMEQHY	72	8		5620
PAP	QLLYLPFR	152	8		5621
PAP	QLTQLGMEQH	69	10		5622
PAP	QLTQLGMEQHY	69	11		5623
PSM	QSGAAVVH	389	8		5624
Kallikrein	QSLRPDEDSSH	109	11		5625
Kallikrein	QVAVYSHGWAH	39	11		5626
PSA	QVFQVSHSFPH	84	11		5627
PSA	QVHPQKVTK	182	9	0.0140	5628
PSA	QVLVASRGR	35	9	0.0018	5629
PSA	QVSHSFPH	87	8		5630
PSA	QVSHSFPHPLY	87	11		5631
PAP	QVYIRSTDVDR	101	11		5632
PAP	RAAPLLLAR	2	9	0.1200	5633
PAP	RATQIPSY	273	8		5634
PAP	RATQIPSYK	273	9	0.0600	5635
PAP	RATQIPSYKK	273	10	0.0250	5636
PSA	RAVCGGVLVH	43	10	0.0310	5637
PSM	RDMKINCSGK	190	10	0.0002	5638
PSM	RDYAVVLR	598	8		5639
PSM	RDYAVVLRK	598	9	0.0190	5640
PSM	RDYAVVLRKY	598	10		5641
PSA	RFLRPGDDSSH	105	11		5642
PAP	RFQELESETLK	163	11		5643
PSM	RGAVEPDR	363	8		5644
PSM	RGAVEPDRY	363	9		5645
PSM	RGSLKVPY	320	8		5646
Kallikrein	RIVGGWECEK	24	10	0.0670	5647
PSA	RIVGGWECEK	20	10	0.0670	5648
Kallikrein	RIVGGWECEKH	24	11		5649
PSA	RIVGGWECEKH	20	11		5650
PSM	RIYNVIGTLR	354	10	0.4300	5651
PSM	RLGIASGR	527	8		5652
PSM	RLGIASGRAR	527	10		5653
PSM	RLGIASGRARY	527	11		5654
PSM	RLLQERGVAY	440	10	0.0005	5655

Table XVII

Prostate A11 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PAP	RNETQHEPY	332	9	0.0002	5656
PSA	RNKSVILLGR	64	10		5657
PSA	RNKSVILLGRH	64	11		5658
PSM	RSFGTLKK	400	8		5659
Kallikrein	RSLQCVSLH	169	9		5660
PAP	RSVLAKELK	28	9	0.1100	5661
PSM	RTEDFFKLER	181	10		5662
PSM	RVDCTPLMY	463	9		5663
Kallikrein	RVPVSHSFPH	89	10		5664
PSM	SAPPDSSWR	312	9	0.0012	5665
PSM	SAVATARR	10	8		5666
PSM	SAVATARRPR	10	10		5667
PAP	SCHLTELY	312	8		5668
PAP	SCHLTELYFEK	312	11		5669
PSM	SFDSLFSAVK	628	10		5670
PSM	SFGTLKKEGWR	401	11		5671
PSM	SGAAVVHEIVR	390	11		5672
PSM	SGKIVIAR	197	8		5673
PSM	SGKIVIARY	197	9		5674
PSM	SGKIVIARYGK	197	11		5675
PAP	SGLQMALDVY	294	10		5676
PSM	SGMPRISK	507	8		5677
PSM	SGNDFEVFFQR	517	11		5678
PSM	SGRARYTK	532	8		5679
PSM	SGYPLYHSVY	547	10		5680
PSM	SHEGNYTLR	455	9		5681
Kallikrein	SHEPEEFLR	159	9		5682
Kallikrein	SHEPEEFLRPR	159	11		5683
PSA	SHEPEEFLTPK	155	11		5684
PSM	SIPVHPIGY	291	9		5685
PSM	SIPVHPIGYY	291	10	1.4000	5686
PSM	SISMKHPQEMK	613	11		5687
PSM	SIVLPFDCR	590	9	0.0220	5688
PSM	SIVLPFDCRDY	590	11		5689
PSM	SLFEPPPPGY	142	10		5690
Kallikrein	SLLKHQSLR	104	9		5691
PSA	SLLKNRFLR	100	9	0.0470	5692
PAP	SLLSLYGHH	242	9	0.0002	5693
PAP	SLLSLYGHHK	242	10	2.3000	5694
Kallikrein	SLQCVSLH	170	8		5695
Kallikrein	SLRPDEDSSH	110	10		5696
PSM	SLVHNLTK	472	8		5697
PSM	SLVHNLTKELK	472	11		5698
PSM	SLYESWTK	492	8		5699
PSM	SLYESWTKK	492	9	2.0000	5700
PAP	SLYGHHKQK	245	9	0.8000	5701

Table XVII

Prostate A11 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PAP	SLYGHIKQKEK	245	11		5702
PSA	SLYTKVVH	237	8		5703
PSA	SLYTKVVHY	237	9	0.0140	5704
PSA	SLYTKVVHYR	237	10	0.2300	5705
PSA	SLYTKVVHYRK	237	11		5706
PSM	SMKHPQEMK	615	9	0.0720	5707
PSM	SMKHPQEMKTY	615	11		5708
Kallikrein	SNDMCARAY	180	9		5709
PSA	SNDVCAQVH	176	9		5710
PSM	SNEATNITPK	46	10		5711
PSM	SNEATNITPKH	46	11		5712
Kallikrein	SSHDLMLLR	117	9	1.2000	5713
PSA	SSHDLMLLR	113	9	1.2000	5714
PSM	SSIEGNYTLR	454	10	0.0910	5715
PSM	SSNEATNITPK	45	11		5716
PSM	SSWRGSLK	317	8		5717
PSM	SSWRGSLKVPY	317	11		5718
PAP	STECMTTNSH	369	10		5719
PSM	STEWAEENSR	431	10	0.0016	5720
PSM	STNEVTRIY	348	9	0.0083	5721
PSM	STQKVKMH	338	8		5722
PSM	STQKVKMHIH	338	10		5723
PSA	SVILLGRH	67	8		5724
PAP	SVLAKELK	29	8	0.0061	5725
PSM	SVYETVELVEK	554	11		5726
PSA	TAAHCIRNK	58	9	0.0140	5727
Kallikrein	TAAHCLKK	62	8		5728
PSM	TDSAVATAR	8	9		5729
PSM	TDSAVATARR	8	10		5730
PAP	TFPTDPIK	52	8		5731
Kallikrein	TGAVPLIQSR	15	10		5732
PSM	TGNFSTQK	334	8		5733
PSM	TGNFSTQKVK	334	10	0.0002	5734
Kallikrein	TGQRVPVSH	86	9		5735
PSA	TGQVFQVSH	82	9	0.0002	5736
PAP	TLGKLSGLH	190	9		5737
PSM	TLKKEGWR	404	8		5738
PSM	TLKKEGWRPR	404	10	0.0002	5739
PSM	TLKKEGWRPRR	404	11		5740
PAP	TLKSEEFQK	171	9	0.0078	5741
PAP	TLKSEEFQKR	171	10	0.0001	5742
PSM	TLRGAVEPDR	361	10	0.0002	5743
PSM	TLRGAVEPDRY	361	11		5744
PSM	TLRVDCTPLMY	461	11		5745
PAP	TLVFRHGDR	39	9	0.0002	5746
PSM	TNEVTRIY	349	8		5747

Table XVII

Prostate A*1101 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PSM	TNITPKTHNMK	50	10		5748
PSM	TNKFSGYPLY	543	10		5749
PSM	TNKFSGYPLYH	543	11		5750
PSM	TSLFEPPPPGY	141	11		5751
PAP	TVPLSEDQLLY	145	11		5752
PSM	VATARRPR	12	8		5753
Kallikrein	VAVYSHGWAH	40	10		5754
PSA	VCAQVHPQK	179	9		5755
PSA	VCGGVLVH	45	8		5756
PSM	VDCTPLMY	464	8		5757
PSM	VDPSKAWGEVK	719	11		5758
PSA	VFQVSHSFPH	85	10		5759
PSM	VFRGNKVK	208	8		5760
Kallikrein	VGGWECEK	26	8		5761
PSA	VGGWECEK	22	8		5762
Kallikrein	VGGWECEKH	26	9		5763
PSA	VGGWECEKH	22	9		5764
PSM	VGLPSPVH	287	9		5765
PSM	VIARYGKVFR	201	10		5766
PSA	VILLGRHSLFH	68	11		5767
PSM	VILYSDPADY	225	10		5768
PSA	VISNDVCAQVH	174	11		5769
PSM	VIYAPSSH	690	8		5770
PSM	VIYAPSSHNK	690	10	0.7900	5771
PSM	VIYAPSSHNKY	690	11		5772
PSM	VLLSYPNK	115	8		5773
PSM	VLLSYPNKTH	115	10		5774
PSM	VLPFDCRDY	592	9		5775
PSM	VLRKYADK	603	8		5776
PSM	VLRKYADKIY	603	10		5777
PSA	VLTAAHCIR	56	9	0.0005	5778
PSA	VLTAAHCIRNK	56	11		5779
Kallikrein	VLTAAHCLK	60	9		5780
Kallikrein	VLTAAHCLKK	60	10		5781
PSA	VLVASRGR	36	8		5782
PAP	VLVNEILNH	262	9	0.0030	5783
PAP	VLVNEILNHMK	262	11		5784
PAP	VNEILNHMK	264	9		5785
PAP	VNEILNHMKR	264	10		5786
PSM	VNYARTEDFFK	177	11		5787
PSM	VSFDSLFSAVK	627	11		5788
PAP	VSGLQMALDVY	293	11		5789
Kallikrein	VSHSFPHPLY	92	10	0.0015	5790
PSA	VSHSFPHPLY	88	10	0.0015	5791
PSA	VTKFMLCAGR	188	10	0.0120	5792
PAP	VTLVFRHGDR	38	10		5793

Table XVII

Prostate A1 I Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
Kallikrein	VVIIYRKWIK	246	9	0.0930	5794
PSA	VVIIYRKWIK	242	9	0.0930	5795
PSM	VVLRKYADK	602	9	0.0660	5796
PSM	VVLRKYADKIY	602	11		5797
Kallikrein	WAIICGGVLVH	47	10		5798
PAP	WATEDTMTK	226	9	0.0002	5799
PAP	WATEDTMTKLR	226	11		5800
PSM	WGEVKRQIY	725	9		5801
Kallikrein	WGPEPCALPEK	229	11		5802
PSA	WGSEPCALPER	225	11		5803
Kallikrein	WGSIEPEEFLR	157	11		5804
PSA	WIGAAPLILSR	10	11		5805
PAP	WLDRSVLAK	25	9	0.0150	5806
PSM	WNLPGGGVQR	246	10		5807
PAP	WSKVYDPLY	206	9	0.0002	5808
PAP	WSTECMTTNSH	368	11		5809
PSA	WVLTAAHCIR	55	10	0.0001	5810
Kallikrein	WVLTAAHCLK	59	10		5811
Kallikrein	WVLTAAHCLKK	59	11		5812
PSM	YADKIYSISMK	607	11		5813
PSM	YAGESFPGIY	700	10		5814
PSM	YAPSSHNK	692	8		5815
PSM	YAPSSHNKY	692	9		5816
PSM	YARTEDFFK	179	9		5817
PAP	YASCHLTELY	310	10	0.0002	5818
PSM	YAVVLRKY	600	8		5819
PSM	YAVVLRKYADK	600	11		5820
PSM	YDALFDIESK	709	10		5821
PSM	YDAQKLLEK	300	9	0.0002	5822
PSA	YDMSLLKNR	97	9		5823
PAP	YDPLYCESVH	210	10		5824
PSM	YDPMFKYH	566	8		5825
PSM	YDVLLSYPNK	113	10	0.0016	5826
PSM	YEAPGVKSY	234	9		5827
PAP	YEVEMYYR	325	8		5828
PAP	YGIHKQKEK	247	9	0.0002	5829
PAP	YGIHKQKEKSR	247	11		5830
PSM	YGKVFRGNK	205	9	0.0002	5831
PSM	YGKVFRGNKVK	205	11		5832
PAP	YIRKRYRK	84	8		5833
PAP	YIRSTDVDR	103	9		5834
PAP	YLPFRNCPR	155	9		5835
PSM	YNFTQIPH	75	8		5836
PAP	YNGLLPPY	303	8		5837
Kallikrein	YNMSLLKH	101	8		5838
PSM	YNVIGTLR	356	8		5839

TABLE XVIC

Prostate A11 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*1101	Seq. Id. No.
PSM	YSLVHNLTK	471	9	0.5400	5840
PSM	YTKNWETNK	537	9		5841
Kallikrein	YTKVVHYR	243	8		5842
PSA	YTKVVHYR	239	8		5843
Kallikrein	YTKVVHYRK	243	9	0.0580	5844
PSA	YTKVVHYRK	239	9	0.0580	5845
PSM	YVILGGHR	371	8		5846

Table XVIII

Prostate A24 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PSM	AFIDPLGL	674	8		5847
PSM	AFLDELKAENI	60	11		5848
PSM	AFTVQAAAETL	736	11		5849
PAP	AMTNLAAL	116	8		5850
PAP	AMTNLAALF	116	9	0.0150	5851
PSM	AWGEVKRQI	724	9		5852
PSM	AYINADSSI	448	9	0.0190	5853
Kallikrein	AYSEKVTEF	187	9		5854
Kallikrein	AYSEKVTEFML	187	11		5855
Kallikrein	CYASGWGSI	152	9	0.1700	5856
PSA	CYASGWGSI	148	9	0.1700	5857
PSM	DFDKSNPI	652	8		5858
PSM	DFDKSNPIVL	652	10		5859
PSM	DFEVFFQRL	520	9		5860
PSM	DFEVFFQRLGI	520	11		5861
PSM	DFFKLERDMKI	184	11		5862
PAP	DFIATLGKL	186	9	0.0002	5863
PSM	DMKINCSGKI	191	10		5864
PSA	DMSLLKNRF	98	9	0.0001	5865
PSA	DMSLLKNRFL	98	10		5866
PSM	EFGLDSVEL	102	9		5867
PSM	EFGLLGSTEW	425	10		5868
Kallikrein	EFLRPRSL	164	8		5869
PSA	EFLTPKKL	160	8		5870
Kallikrein	EFMLCAGL	194	8		5871
Kallikrein	EFMLCAGLW	194	9		5872
PSM	EFSGMPRI	505	8		5873
PSM	EFSGMPRISKL	505	11		5874
PSM	EMKTYSVSF	621	9	0.0010	5875
PSM	EWAEENSRL	433	9		5876
PSM	EWAEENSRLL	433	10		5877
PSM	EYAYRRGI	276	8		5878
PAP	EYIRKRYRKF	83	10	0.0067	5879
PAP	EYIRKRYRKFL	83	11		5880
PSM	FFKLERDMKI	185	10		5881
PSM	FFLLGFLF	32	8		5882
PSM	FFLLGFLFGW	32	10	0.0026	5883
PSM	FFLLGFLFGWF	32	11		5884
PAP	FFWLDRSVL	23	9	0.0017	5885
Kallikrein	FMLCAGLW	195	8		5886
PSA	FMLCAGRW	191	8		5887
PAP	FWLDRSVL	24	8		5888
PSM	FYDPMFKYHL	565	10	1.1000	5889
PSM	GFEGKSLYESW	487	11		5890
PSM	GFFLLGFL	31	8		5891
PSM	GFFLLGFLF	31	9	0.0190	5892

Table XVII

Prostate A24 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PSM	GFFLLGFLFGW	31	11		5893
PAP	GFGQLTQL	66	8		5894
PSM	GFLFGWFI	36	8		5895
PAP	GFLFLLFF	17	8		5896
PAP	GFLFLLFFW	17	9	0.0016	5897
PAP	GFLFLLFFWL	17	10	0.0007	5898
PAP	GMEQHYEL	74	8		5899
PSM	GMPRISKL	508	8		5900
PSM	GMVFELANSI	582	10	0.0002	5901
Kallikrein	GWAHCGGVL	46	9		5902
Kallikrein	GWECEKHSQPW	28	11		5903
PSA	GWECEKHSQPW	24	11		5904
Kallikrein	GWGSIEPEEF	156	10	0.0001	5905
PSA	GWGSIEPEEF	152	10	0.0001	5906
Kallikrein	GWGSIEPEEFL	156	11		5907
PSA	GWGSIEPEEFL	152	11		5908
PSM	GWRPRRTI	409	8		5909
PSM	GWRPRRTIL	409	9		5910
PSM	GWRPRRTILF	409	10	0.0540	5911
PSM	GYENVSDI	150	8		5912
PSM	GYYDAQKL	298	8		5913
PSM	GYYDAQKLL	298	9		5914
PAP	HMKRATQI	270	8		5915
PAP	HYELGEYI	78	8		5916
Kallikrein	HYRKWIKDTI	248	10	0.0550	5917
PSA	HYRKWIKDTI	244	10	0.0550	5918
PAP	IWNPILLW	131	8		5919
PAP	IWNPILLWQPI	131	11		5920
PAP	IWSKVYDPL	205	9	0.0024	5921
PSM	IYDALFDI	708	8		5922
PSM	IYNVIGTL	355	8		5923
PSM	KFLYNFTQI	72	9		5924
PSA	KFMLCAGRW	190	9	0.0310	5925
PSM	KFSERLQDF	645	9		5926
PSM	KFYDPMFKYHL	564	11		5927
PSM	KYADKIYSI	606	9	12.0000	5928
PSM	KYAGESFPGI	699	10		5929
PSM	LFASWDAEEF	417	10		5930
PAP	LFFWLDRSVL	22	10	0.0045	5931
PSA	LFHPEDTGQVF	76	11		5932
PAP	LFLLFFWL	19	8		5933
PAP	LFPPEGVSI	123	9	0.0033	5934
PAP	LFPPEGVSIW	123	10	0.0140	5935
PSM	LFSAVKNF	632	8		5936
PSM	LFSAVKNFTEI	632	11		5937
PSM	LMFLERAF	668	8		5938

Table XVIIIC

Prostate A24 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PSM	LMFLERAFI	668	9	0.0075	5939
PAP	LMSAMTNL	113	8		5940
PAP	LMSAMTNLAAL	113	11		5941
PSM	LMYSLVHNL	469	9		5942
PAP	LYCESVHNF	213	9	0.4400	5943
PAP	LYCESVHNFTL	213	11		5944
PSA	LYDMSLLKNRF	96	11	0.1200	5945
PAP	LYFEKGEYF	318	9	2.5000	5946
PSM	LYHSVYETYEL	551	11		5947
PAP	LYLPFRNCPRF	154	11		5948
PSM	LYNFTQIPHL	74	10	0.2300	5949
PSM	LYSDPADYF	227	9	0.4400	5950
PSA	LYTKVVHYRKW	238	11		5951
PSM	MFLERAFI	669	8		5952
PSM	MFLERAFIDPL	669	11		5953
PSM	MMNDQLMF	663	8		5954
PSM	MMNDQLMFL	663	9		5955
Kallikrein	MWDLVLSI	1	8		5956
Kallikrein	MWDLVLSIAL	1	10		5957
PSM	MYSLVHNL	470	8		5958
PSM	NFQLAKQI	89	8		5959
PSM	NFSTQKVKMHI	336	11		5960
PSM	NFTEIASKF	638	9	0.0001	5961
PSM	NFTQIPHL	76	8		5962
PSM	NMKAFLDEL	57	9		5963
Kallikrein	NMSLLKHQSL	102	10		5964
PSM	NYARTEDF	178	8		5965
PSM	NYARTEDFF	178	9	0.7700	5966
PSM	NYARTEDFFKL	178	11		5967
PSM	NYTLRVDCTPL	459	11		5968
PSM	PFDCRDYAVVL	594	11		5969
PAP	PFRNCPRF	157	8		5970
PAP	PFRNCPRFQEL	157	11		5971
Kallikrein	PWQVAVYSHGW	37	11		5972
PAP	PYASCHLTEL	309	10	0.0240	5973
PAP	PYKDFIATL	183	9	0.1100	5974
PSM	PYNVGPGF	326	8		5975
PAP	QMALDVYNGL	297	10	0.0001	5976
PAP	QMALDVYNGLL	297	11		5977
PSA	QWVLTAAHCI	54	10	0.0007	5978
Kallikrein	QWVLTAAHCL	58	10		5979
PAP	RFAELVGPVI	355	10	0.0037	5980
PAP	RFQELESETL	163	10	0.0001	5981
PSM	RMMNDQLMF	662	9		5982
PSM	RMMNDQLMFL	662	10		5983
PSM	RWLCAGAL	19	8		5984

Table XVIII

Prostate A24 Motif Peptides with Binding Data

Protein	Sequence	Position	No. of Amino Acids	A*2401	Seq. Id. No.
PSM	RWLCAGALVL	19	10		5985
PSM	RYTKNWETNKF	536	11		5986
PSM	SFGTLKKEGW	401	10		5987
PSM	SFPGIYDAL	704	9		5988
PSM	SFPGIYDALF	704	10		5989
PSA	SFPHPLYDMSL	91	11		5990
Kallikrein	SFPHPLYNMSL	95	11		5991
PAP	SWATEDTMTKL	225	11		5992
PSM	SWDAEEFGL	420	9		5993
PSM	SWDAEEFGLL	420	10		5994
Kallikrein	SWGPEPCAL	228	9		5995
PSA	SWGSEPCAL	224	9	0.0001	5996
PAP	SWPQGFGQL	62	9	0.0013	5997
PSM	SWTKKSPSPEF	496	11		5998
PAP	SYKHEQVYI	96	9	0.2600	5999
PSM	SYPDGWNL	241	8		6000
PSM	SYPNKTHPNYI	118	11		6001
PAP	TMTKLREL	231	8		6002
PAP	TMTKLRELSEL	231	11		6003
PSA	TWIGAAPL	9	8		6004
PSA	TWIGAAPLI	9	9	0.1100	6005
PSA	TWIGAAPLIL	9	10	0.3600	6006
PSM	TYELVEKF	558	8		6007
PSM	TYSVSFDSL	624	9		6008
PSM	TYSVSFDSLF	624	10	3.2000	6009
PSM	VFELANSI	584	8		6010
PSM	VFELANSIVL	584	10		6011
PSM	VFFQRLGI	523	8		6012
PSA	VFLTLSVTW	2	9	2.1000	6013
PSA	VFLTLSVTWI	2	10	0.0062	6014
PSA	VFQVSHSF	85	8		6015
PSA	VFRHGDRSPI	41	10	0.0005	6016
PAP	VMDLPTQEPAL	134	11		6017
PSA	VWLGRHNL	73	8		6018
Kallikrein	VWLGRHNLF	73	9		6019
Kallikrein	VYETYELVEKF	555	11		6020
PSM	VYTKVVHYRKW	242	11		6021
Kallikrein	VYVNYARTEDF	175	11		6022
PSM	YFEKGEYF	319	8		6023
PAP	YYDAQKLL	299	8		6024
PSM					

Table XIX

Prostate DR Supermotif Peptides

Protein	Sequence	Seq. Id. No.	Core Sequence	Core Seq. Id. No	Position
PAP	---MRAAPLLLARAA	6025	MRAAPLLLA	6300	1
Kallikrein	---MWDLVLSIALSV	6026	MWDLVLSIA	6301	1
PSA	---VVFLTLSVTWIG	6027	VVFLTLSVT	6302	1
Kallikrein	--MWDLVLSIALSVG	6028	WDLVLSIAL	6303	2
PSA	--VVFLTLSVTWIGA	6029	VFLTLSVTW	6304	2
PSA	-VVFLTLSVTWIGAA	6030	FLTLSVTWI	6305	3
PAP	AALFPPEGVSIWNPI	6031	FPPEGVSIW	6306	124
PSA	AAPLILSRIVGGWEC	6032	LILSRIVGG	6307	16
PAP	AAPLLLARAASLSLG	6033	LLLARAASL	6308	6
PAP	AASLSLGFLFLLFFW	6034	LSLGFLFLL	6309	14
PSM	ADKIYSISMKHPQEM	6035	IYSISMKHP	6310	611
PSM	AEAVGLPSIPVHPIG	6036	VGLPSIPVH	6311	287
PSM	AEEFGLLGSTEWAEE	6037	FGLLGSTEW	6312	426
PAP	AELVGPVIPQDWSTE	6038	VGPVIPQDW	6313	360
PSA	AGRWTGGKSTCSGDS	6039	WTGGKSTCS	6314	198
PSA	AHCIRNKSVILLGRH	6040	IRNKSVILL	6315	63
PAP	AKELKFVTLVFRHGD	6041	LKFVTLVFR	6316	35
PAP	ALDVYNGLLPPYASC	6042	VYNGLLPPY	6317	302
Kallikrein	ALSVGCTGAVPLIQS	6043	VGCTGAVPL	6318	12
PSA	APLILSRIVGGWECE	6044	ILSRIVGGW	6319	17
PAP	APLLLARAASLSLGF	6045	LLARAASLS	6320	7
Kallikrein	ARAYSEKVTEFMLCA	6046	YSEKVTEFM	6321	188
Kallikrein	ASGWGSIEPEEFLRP	6047	WGSIEPEEF	6322	157
PSA	ASGWGSIEPEEFLTP	6048	WGSIEPEEF	6323	153
PSM	AVGLPSIPVHPIGYY	6049	LPSIPVHPI	6324	289
PSA	AVKVMDLPTQEPALG	6050	VMDLPTQEP	6325	134
Kallikrein	AVPLIQSRIVGGWEC	6051	LIQSRIVGG	6326	20
PSA	CAQVHPQKVTKFMLC	6052	VHPQKVTKF	6327	183
PAP	CESVHNFTLPSWATE	6053	VHNFTLPSW	6328	218
Kallikrein	CNGVLQGITSWGPEP	6054	VLQGITSWG	6329	222
PSA	CNGVLQGITSWGSEP	6055	VLQGITSWG	6330	218
PAP	CPRFQELESETLKSE	6056	FQELESETL	6331	164
PSM	CTPLMYSLVHNLTKE	6057	LMYSLVHNL	6332	469
PSM	DEGFEGKSLYESWTK	6058	FEGKSLYES	6333	488
PSM	DFEVFFQRLGIASGR	6059	VFFQRLGIA	6334	523
PSA	DLHVISNDVCAQVHP	6060	VISNDVCAQ	6335	174
Kallikrein	DLVLSIALSVGCTGA	6061	LSIALSVGC	6336	6
PSM	DPMFKYHLTVAQVRG	6062	FKYHLTVAQ	6337	570
PSM	DQLMFLERAFIDPLG	6063	MFLERAFID	6338	669
PSM	DRPFYRHVIYAPSSH	6064	FYRHVIYAP	6339	686
PAP	DRSVLAKELKFVTLV	6065	VLAKELKFV	6340	30
PAP	DRTLMSAMTNLAALF	6066	LMSAMTNLA	6341	113
PSM	DSSIEGNYTLRVDCT	6067	IEGNYTLRV	6342	456
PAP	DTTVSGLQMALDVYN	6068	VSGLQMALD	6343	293
Kallikrein	EEFLRPRSLQCVSLH	6069	LRPRSLQCV	6344	166
PSA	EEFLTPKKLQCVDLH	6070	LTPKKLQCV	6345	162

Table XIX

Prostate DR Supermotif Peptides

Protein	Sequence	Seq. Id. No.	Core Sequence	Core Seq. Id. No	Position
PSM	EFGLDSVELAHYDVL	6071	LDSVELAHY	6346	105
PSM	ERDMKINCSGKIVIA	6072	MKINCSGKI	6347	192
PSM	ERGVAYINADSSIEG	6073	VAYINADSS	6348	447
PSM	ESKVDPSKAWGEVKR	6074	VDPSKAWGE	6349	719
PSM	EVFFQRLGIASGRAR	6075	FQRLGIASG	6350	525
PSM	EYAYRRGIAEAVGLP	6076	YRRGIAEAV	6351	279
PAP	FAELVGPVIPQDWST	6077	LVGPVIPQD	6352	359
PAP	FFWLDRSVLAKELKF	6078	LDRSVLAKE	6353	26
PAP	FGQLTQLGMEQHYEL	6079	LTQLGMEQH	6354	70
PAP	FLFLLFFWLDRSVLA	6080	LLFFWLDRS	6355	21
PSA	FLTLSVTWIGAAPLI	6081	LSVTWIGAA	6356	6
PAP	FQELESETLKSEEFQ	6082	LESETLKSE	6357	167
PSM	FSAFSPQGMPEGDLV	6083	FSPQGMPEG	6358	164
PSM	FSGYPLYHSVYETYE	6084	YPLYHSVYE	6359	549
PSM	FTEIASKFSERLQDF	6085	IASKFSERL	6360	642
PSM	GAAVVHEIVRSFGTL	6086	VVHEIVRSF	6361	394
PSM	GDLVYVNYARTEDFF	6087	VYVNYARTE	6362	175
PSM	GDPLTPGYPANEYAY	6088	LTPGYPANE	6363	268
PSM	GGFFLLGFLFGWFIK	6089	FLLGFLFGW	6364	33
PSM	GGGVQRGNILNLNGA	6090	VQRGNILNL	6365	253
PSA	GGPLVCNGVLQGITS	6091	LVCNGVLQG	6366	213
Kallikrein	GGPLVCNGVLQGITS	6092	LVCNGVLQG	6367	217
PAP	GGVLVNEILNHMKRA	6093	LVNEILNHM	6368	263
PSM	GKSLYESWTKKSPSP	6094	LYESWTKKS	6369	493
PSM	GKVFRGNKVKNAQLA	6095	FRGNKVKNA	6370	209
PSM	GMVFELANSIVLPFD	6096	FELANSIVL	6371	585
PSM	GNEIFNTSLFEPPPP	6097	IFNTSLFEP	6372	138
PSM	GNILNLNGAGDPLTP	6098	LNLNGAGDP	6373	259
PSM	GNKVKNAQLAGAKGV	6099	VKNAQLAGA	6374	214
PSM	GPGFTGNFSTQKVKM	6100	FTGNFSTQK	6375	333
PSA	GPLVCNGVLQGITSW	6101	VCNGVLQGI	6376	214
Kallikrein	GPLVCNGVLQGITSW	6102	VCNGVLQGI	6377	218
PAP	GPVIPQDWSTECMTT	6103	IPQDWSTEC	6378	364
PAP	GQDLFGIWSKVYDPL	6104	LFGIWSKVY	6379	202
Kallikrein	GQRVPVSHSFPHPLY	6105	VPVSHSFPH	6380	90
PSA	GQVFQVSHSFPHPLY	6106	FQVSHSFPH	6381	86
PSA	GRAVCGGVLVHPQWV	6107	VCGGVLVHP	6382	45
PSM	GVAYINADSSIEGNY	6108	YINADSSIE	6383	449
PSM	GVILYSDPADYFAPG	6109	LYSDPADYF	6384	227
PSA	GVLVHPQWVLTAAHC	6110	VHPQWVLTA	6385	51
Kallikrein	GVLVHPQWVLTAAHC	6111	VHPQWVLTA	6386	55
PAP	GVSIWNPILLWQPIP	6112	IWNPILLWQ	6387	131
PSM	GWNLPGGGVQRGNIL	6113	LPGGGVQRG	6388	248
PSA	HDLMLLRLSEPAELT	6114	MLLRLSEPA	6389	118
Kallikrein	HDLMLLRLSEPAKIT	6115	MLLRLSEPA	6390	122
PSM	HEIVRSFGTLKKEGW	6116	VRSFGTLKK	6391	399

Table XIX
Prostate DR Supermotif Peptides

Protein	Sequence	Seq. Id. No.	Core Sequence	Core Seq. Id. No	Position
PAP	HEPYPLMLPGCSPSC	6117	YPLMLPGCS	6392	340
PAP	HEQVYIRSTDVDRTL	6118	VYIRSTDVD	6393	102
Kallikrein	HNLFEPEDTGQRVPV	6119	FEPEDTGQR	6394	81
PSA	HPLYDMSLLKNRFLR	6120	YDMSLLKNR	6395	97
Kallikrein	HPLYNMSLLKHQSLR	6121	YNMSLLKHQ	6396	101
PSA	HPQWVLTAAHCIRNK	6122	WVLTAAHCI	6397	55
Kallikrein	HPQWVLTAAHCLKKN	6123	WVLTAAHCL	6398	59
PSA	HSLFHPEDTGQVFQV	6124	FHPEDTGQV	6399	77
PSM	HSVYETYELVEKFYD	6125	YETYELVEK	6400	556
PSM	HYDVLLSYPNKTHPN	6126	VLLSYPNKT	6401	115
PAP	IDTFPTDPIKESSWP	6127	FPTDPIKES	6402	53
PSM	IGYYDAQKLLEKMGG	6128	YDAQKLLEK	6403	300
PSM	IKKFLYNFTQIPHLA	6129	FLYNFTQIP	6404	73
PAP	ILLWQPIPVHTVPLS	6130	WQPIPVHTV	6405	138
PAP	IPSYKKLIMYSAHDT	6131	YKKLIMYSA	6406	280
Kallikrein	ITSWGPEPCALPEKP	6132	WGPEPCALP	6407	229
PSA	ITSWGSEPCALPERP	6133	WGSEPCALP	6408	225
PSM	IYSISMKHPQEMKTY	6134	ISMKHPQEM	6409	614
PSM	KAFLDELKAENIKKF	6135	LDELKAENI	6410	62
PSM	KEGWRPRRTILFASW	6136	WRPRRTILF	6411	410
PSM	KFLYNFTQIPHLAGT	6137	YNFTQIPHL	6412	75
PSM	KGVILYSDPADYFAP	6138	ILYSDPADY	6413	226
Kallikrein	KPAVYTKVVHYRKWI	6139	VYTKVVHYR	6414	242
PAP	KSRLQGGVLVNEILN	6140	LQGGVLVNE	6415	258
PSM	KVKMHIHSTNEVTRI	6141	MHIHSTNEV	6416	344
PSM	KYHLTVAQVRGGMVF	6142	LTVAQVRGG	6417	574
PSM	LAHYDVLLSYPNKTH	6143	YDVLLSYPN	6418	113
PSM	LDELKAENIKKFLYN	6144	LKAENIKKF	6419	65
PAP	LDVYNGLLPPYASCH	6145	YNGLLPPYA	6420	303
PSM	LEKMGGSAPPDSSWR	6146	MGGSAPPDS	6421	309
PAP	LFFWLDRSVLAKELK	6147	WLDRSVLAK	6422	25
PSM	LFGWFIKSSNEATNI	6148	WFIKSSNEA	6423	41
PSM	LGFLFGWFIKSSNEA	6149	LFGWFIKSS	6424	38
Kallikrein	LHLLSNDMCARAYSE	6150	LSNDMCARA	6425	179
PAP	LHPYKDFIATLGKLS	6151	YKDFIATLG	6426	184
PSA	LHVISNDVCAQVHPQ	6152	ISNDVCAQV	6427	175
PAP	LIMYSAHDTTVSGLQ	6153	YSAHDTTVS	6428	286
PAP	LLFFWLDRSVLAKEL	6154	FWLDRSVLA	6429	24
PAP	LLYLPFRNCPRFQEL	6155	LPFRNCPRF	6430	156
PSM	LMFLERAFIDPLGLP	6156	LERAFIDPL	6431	671
PSA	LMLLRLSEPAELTDA	6157	LRLSEPAEL	6432	120
Kallikrein	LMLLRLSEPAKITDV	6158	LRLSEPAKI	6433	124
PAP	LPPYASCHLTELYFE	6159	YASCHLTEL	6434	310
PSM	LPSIPVHPIGYYDAQ	6160	IPVHPIGYY	6435	292
PAP	LPSWATEDTMTKLRE	6161	WATEDTMTK	6436	226
PSA	LQCVDLHVISNDVCA	6162	VDLHVISND	6437	170

Table XIX

Prostate DR Supermotif Peptides

Protein	Sequence	Seq. Id. No.	Core Sequence	Core Seq. Id. No	Position
Kallikrein	LQCVSLHLLSNDMCA	6163	VSLHLLSND	6438	174
PSM	LQDFDKSNPIVLRMM	6164	FDKSNPIVL	6439	653
Kallikrein	LQGITSWGPEPCALP	6165	ITSWGPEPC	6440	226
PSA	LQGITSWGSEPCALP	6166	ITSWGSEPC	6441	222
PAP	LRELSELSLLSLYGI	6167	LSELSLLSL	6442	238
PSM	LRMMNDQLMFLERAF	6168	MNDQLMFLE	6443	664
PAP	LSELSLLSLYGIHKQ	6169	LSLLSLYGI	6444	241
PAP	LSGLHGQDLFGIWSK	6170	LHGQDLFGI	6445	197
PAP	LSLLSLYGIHKQKEK	6171	LSLYGIHKQ	6446	244
PSM	LVYVNYARTEDFFKL	6172	VNYARTEDF	6447	177
PSM	MFKYHLTVAQVRGGM	6173	YHLTVAQVR	6448	572
PSM	MPRISKLGSGNDFEV	6174	ISKLGSGND	6449	512
PAP	MSAMTNLAALFPPEG	6175	MTNLAALFP	6450	117
Kallikrein	MSLLKHQSLRPDEDS	6176	LKHQSLRPD	6451	106
PSA	MSLLKNRFLRPGDDS	6177	LKNRFLRPG	6452	102
PAP	MTNLAALFPPEGVSI	6178	LAALFPPEG	6453	120
Kallikrein	MWDLVLSIALSVGCT	6179	LVLSIALSV	6454	4
PSM	MYSLVHNLTKELKSP	6180	LVHNLTKEL	6455	473
PAP	NESYKHEQVYIRSTD	6181	YKHEQVYIR	6456	97
PAP	NFTLPSWATEDTMTK	6182	LPSWATEDT	6457	223
PAP	NGLLPPYASCHLTEL	6183	LPPYASCHL	6458	307
Kallikrein	NGVLQGITSWGPEPC	6184	LQGITSWGP	6459	223
PSA	NGVLQGITSWGSEPC	6185	LQGITSWGS	6460	219
Kallikrein	NMSLLKHQSLRPDED	6186	LLKHQSLRP	6461	105
PAP	NPLLWQPIPVHTVP	6187	LLWQPIPVH	6462	136
PSM	NSIVLPFDCRDYAVV	6188	VLPFDCRDY	6463	592
PSM	NTSLFEPPPPGYENV	6189	LFEPPPPGY	6464	143
PSM	NYTLRVDCTPLMYSL	6190	LRVDCTPLM	6465	462
PSM	PADYFAPGVKSYPDG	6191	YFAPGVKSY	6466	234
Kallikrein	PCALPEKPAVYTKVV	6192	LPEKPAVYT	6467	236
PSA	PCALPERPSLYTKVV	6193	LPERPSLYT	6468	232
Kallikrein	PEEFLRPRSLQCVSL	6194	FLRPRSLQC	6469	165
PAP	PEGVSIWNPILLWQP	6195	VSIWNPILL	6470	129
PSA	PHPLYDMSLLKNRFL	6196	LYDMSLLKN	6471	96
Kallikrein	PHPLYNMSLLKHQSL	6197	LYNMSLLKH	6472	100
PAP	PILLWQPIPVHTVPL	6198	LWQPIPVHT	6473	137
PAP	PIPVHTVPLSEDQLL	6199	VHTVPLSED	6474	143
PSA	PKKLQCVDLHVISND	6200	LQCVDLHVI	6475	167
PAP	PLLLARAASLSLGFL	6201	LARAASLSL	6476	8
PAP	PLMLPGCSPSCPLER	6202	LPGCSPSCP	6477	344
PAP	PQDWSTECMTTNSHQ	6203	WSTECMTTN	6478	368
PSM	PQEMKTYSVSFDSLF	6204	MKTYSVSFD	6479	622
PSM	PQGMPEGDLVYVNYA	6205	MPEGDLVYV	6480	169
PSA	PQKVTKFMLCAGRWT	6206	VTKFMLCAG	6481	188
Kallikrein	PRSLQCVSLHLLSND	6207	LQCVSLHLL	6482	171
PSM	PRWLCAGALVLAGGF	6208	LCAGALVLA	6483	21

Table XIX

Prostate DR Supermotif Peptides

Protein	Sequence	Seq. Id. No.	Core Sequence	Core Seq. Id. No	Position
PSM	PYNVGPGFTGNFSTQ	6209	VGPGFTGNF	6484	329
PAP	PYPLMLPGCSPSCPL	6210	LMLPGCSPS	6485	342
PAP	QGGVLVNEILNHMKR	6211	VLVNEILNH	6486	262
PSM	QIYVAAFTVQAAAET	6212	VAAFTVQAA	6487	734
PSM	QSQWKEFGLDSVELA	6213	WKEFGLDSV	6488	100
Kallikrein	QVWLGRHNLFEPEDT	6214	LGRHNLFEP	6489	75
PAP	QVYIRSTDVDRTLMS	6215	IRSTDVDRT	6490	104
PSA	QWVLTAAHCIRNKSV	6216	LTAAHCIRN	6491	57
Kallikrein	QWVLTAAHCLKKNSQ	6217	LTAAHCLKK	6492	61
PSM	RAFIDPLGLPDRPFY	6218	IDPLGLPDR	6493	676
PSM	RDSWVFGGIDPQSGA	6219	WVFGGIDPQ	6494	381
PSM	RGGMVFELANSIVLP	6220	MVFELANSI	6495	583
PSM	RHIVIYAPSSHNKYAG	6221	IYAPSSHNK	6496	691
Kallikrein	RKWIKDTIAANP---	6222	IKDTIAANP	6497	253
PSA	RKWIKDTIVANP---	6223	IKDTIVANP	6498	249
PSM	RLGIASGRARYTKNW	6224	IASGRARYT	6499	530
PSM	RPRWLCAGALVLAGG	6225	WLCAGALVL	6500	20
PSA	RPSLYTKVVHYRKWI	6226	LYTKVVHYR	6501	238
PSM	RQIYVAAFTVQAAAE	6227	YVAAFTVQA	6502	733
PAP	RSPIDTFPTDPIKES	6228	IDTFPTDPI	6503	50
Kallikrein	RVPVSHSFPHPLYNM	6229	VSHSFPHPL	6504	92
PSM	SDIVPPFSAFSPQGM	6230	VPPFSAFSP	6505	158
Kallikrein	SEKVTEFMLCAGLWT	6231	VTEFMLCAG	6506	192
PSA	SHDLMLLRLSEPAEL	6232	LMLLRLSEP	6507	117
Kallikrein	SHDLMLLRLSEPAKI	6233	LMLLRLSEP	6508	121
Kallikrein	SIALSVGCTGAVPLI	6234	LSVGCTGAV	6509	10
PAP	SKVYDPLYCESVHNF	6235	YDPLYCESV	6510	210
Kallikrein	SLHLLSNDMCARAYS	6236	LLSNDMCAR	6511	178
PAP	SLSLGFLFLLFFWLD	6237	LGFLFLLFF	6512	16
PSM	SNPIVLRMMNDQLMF	6238	IVLRMMNDQ	6513	659
PSA	SQPWQVLVASRGRAV	6239	WQVLVASRG	6514	34
PSA	SRIVGGWECEKHSQP	6240	VGGWECEKH	6515	22
Kallikrein	SRIVGGWECEKHSQP	6241	VGGWECEKH	6516	26
PSM	SRLLQERGVAYINAD	6242	LQERGVAYI	6517	442
PAP	STDVDRTLMSAMTNL	6243	VDRTLMSAM	6518	109
PSM	STEWAEENSRLLQER	6244	WAEENSRLL	6519	434
PSM	SVELAHYDVLLSYPN	6245	LAHYDVLLS	6520	110
PSA	SVILLGRHSLFHPED	6246	LLGRHSLFH	6521	70
PSM	SVSFDSLFSAVKNFT	6247	FDSLFSAVK	6522	629
PSA	SVTWIGAAPLILSRI	6248	WIGAAPLIL	6523	10
PSM	SWVFGGIDPQSGAAV	6249	FGGIDPQSG	6524	383
PSA	TDAVKVMDLPTQEPA	6250	VKVMDLPTQ	6525	132
Kallikrein	TDVVKVLGLPTQEPA	6251	VKVLGLPTQ	6526	136
Kallikrein	TEFMLCAGLWTGGKD	6252	MLCAGLWTG	6527	196
Kallikrein	TGAVPLIQSRIVGGW	6253	VPLIQSRIV	6528	18
PSM	TGNFSTQKVKMHIHS	6254	FSTQKVKMH	6529	337

Table XIX

Prostate DR Supermotif Peptides

Protein	Sequence	Seq. Id. No.	Core Sequence	Core Seq. Id. No	Position
PSM	TILFASWDAEEFGLL	6255	FASWDAEEF	6530	418
PSM	TLRVDCTPLMYSLVH	6256	VDCTPLMYS	6531	464
PSA	TLSVTWIGAAPLILS	6257	VTWIGAAPL	6532	8
PSM	TNKFSGYPLYHSVYE	6258	FSGYPLYHS	6533	546
PSM	TRIYNVIGTLRGAVE	6259	YNVIGTLRG	6534	356
PSM	TSLFEPPPPGYENVS	6260	FEPPPPGYE	6535	144
PAP	TVPLSEDQLLYLPFR	6261	LSEDQLLYL	6536	148
PSM	TYSVSFDSLFSAVKN	6262	VSFDSLFSA	6537	627
PSM	VAAFTVQAAAETLSE	6263	FTVQAAAET	6538	737
PSM	VAQVRGGMVFELANS	6264	VRGGMVFEL	6539	579
Kallikrein	VAVYSHGWAHCGGVL	6265	YSHGWAHCG	6540	43
PSM	VAYINADSSIEGNYT	6266	INADSSIEG	6541	450
PAP	VEMYYRNETQHEPYP	6267	YYRNETQHE	6542	330
PSM	VFELANSIVLPFDCR	6268	LANSIVLPF	6543	587
PSA	VFQVSHSFPHPLYDM	6269	VSHSFPHPL	6544	88
PSM	VHPIGYYDAQKLLEK	6270	IGYYDAQKL	6545	297
PSA	VILLGRHSLFHPEDT	6271	LGRHSLFHP	6546	71
PSM	VKNFTEIASKFSERL	6272	FTEIASKFS	6547	639
Kallikrein	VLGLPTQEPALGTTC	6273	LPTQEPALG	6548	141
PSM	VLRMMNDQLMFLERA	6274	MMNDQLMFL	6549	663
PSA	VMDLPTQEPALGTTC	6275	LPTQEPALG	6550	137
Kallikrein	VPLIQSRIVGGWECE	6276	IQSRIVGGW	6551	21
PSM	VPPFSAFSPQGMPEG	6277	FSAFSPQGM	6552	161
PSM	VSDIVPPFSAFSPQG	6278	IVPPFSAFS	6553	157
PAP	VSIWNPILLWQPIPV	6279	WNPILLWQP	6554	132
PSA	VTWIGAAPLILSRIV	6280	IGAAPLILS	6555	11
PSA	VVFLTLSVTWIGAAP	6281	LTLSVTWIG	6556	4
Kallikrein	VVKVLGLPTQEPALG	6282	VLGLPTQEP	6557	138
Kallikrein	WDLVLSIALSVGCTG	6283	VLSIALSVG	6558	5
PSM	WKEFGLDSVELAHYD	6284	FGLDSVELA	6559	103
PSM	WNLLHETDSAVATAR	6285	LHETDSAVA	6560	5
PAP	WNPILLWQPIPVHTV	6286	ILLWQPIPV	6561	135
PAP	WQPIPVHTVPLSEDQ	6287	IPVHTVPLS	6562	141
PSM	YAVVLRKYADKIYSI	6288	VLRKYADKI	6563	603
PSM	YDALFDIESKVDPSK	6289	LFDIESKVD	6564	712
PAP	YDPLYCESVHNFTLP	6290	LYCESVHNF	6565	213
PSM	YDPMFKYHLTVAQVR	6291	MFKYHLTVA	6566	569
PSM	YENVSDIVPPFSAFS	6292	VSDIVPPFS	6567	154
PSM	YESWTKKSPSPEFSG	6293	WTKKSPSPE	6568	497
PAP	YKKLIMYSAHDTTVS	6294	LIMYSAHDT	6569	283
PAP	YNGLLPPYASCHLTE	6295	LLPPYASCH	6570	306
PAP	YPLMLPGCSPSCPLE	6296	MLPGCSPSC	6571	343
PSM	YRHVIYAPSSHNKYA	6297	VIYAPSSHN	6572	690
Kallikrein	YRKWIKDTIAANP--	6298	WIKDTIAAN	6573	252
PSA	YRKWIKDTIVANP--	6299	WIKDTIVAN	6574	248

Table XIX

Prostate DR 3a Submotif Peptides

Protein	Sequence	Seq. Id. No.	Core Sequence	Core Seq. Id. No	Position
PAP	AALFPPEGVSIWNPI	6575	FPPEGVSIW	6615	124
PSM	DQLMFLERAFIDPLG	6576	MFLERAFID	6616	669
PSM	EDFFKLERDMKINCS	6577	FKLERDMKI	6617	186
PAP	EMYYRNETQHEPYPL	6578	YRNETQHEP	6618	331
PSM	FGTLKKEGWRPRRTI	6579	LKKEGWRPR	6619	405
PAP	FQELESETLKSEEFQ	6580	LESETLKSE	6620	167
PSM	GAAVVHEIVRSFGTL	6581	VVHEIVRSF	6621	394
PAP	GGVLVNEILNHMKRA	6582	LVNEILNHM	6622	263
PAP	GLQMALDVYNGLLPP	6583	MALDVYNGL	6623	298
PAP	GPVIPQDWSTECMTT	6584	IPQDWSTEC	6624	364
PSM	GVILYSDPADYFAPG	6585	LYSDPADYF	6625	227
PSM	HNKYAGESFPGIYDA	6586	YAGESFPGI	6626	700
Kallikrein	HNLFEPEDTGQRVPV	6587	FEPEDTGQR	6627	81
Kallikrein	HQSLRPDEDSSHDLM	6588	LRPDEDSSH	6628	111
PSA	HSLFHPEDTGQVFQV	6589	FHPEDTGQV	6629	77
PAP	IDTFPTDPIKESSWP	6590	FPTDPIKES	6630	53
PSM	ISHNEDGNEIFNTS	6591	INEDGNEIF	6631	131
PAP	KGEYFVEMYYRNETQ	6592	YFVEMYYRN	6632	325
PSM	LDELKAENIKKFLYN	6593	LKAENIKKF	6633	65
Kallikrein	LHLLSNDMCARAYSE	6594	LSNDMCARA	6634	179
PSA	LHVISNDVCAQVHPQ	6595	ISNDVCAQV	6635	175
PAP	LLFFWLDRSVLAKEL	6596	FWLDRSVLA	6636	24
PAP	LTELYFEKGEYFVEM	6597	LYFEKGEYF	6637	318
PSM	MWNLLHETDSAVATA	6598	LLHETDSAV	6638	4
PAP	NESYKHEQVYIRSTD	6599	YKHEQVYIR	6639	97
PSM	NSRLLQERGVAYINA	6600	LLQERGVAY	6640	441
PSM	NYTLRVDCTPLMYSL	6601	LRVDCTPLM	6641	462
PSM	RGAVEPDRYVILGGH	6602	VEPDRYVIL	6642	366
PSM	RGGMVFELANSIVLP	6603	MVFELANSI	6643	583
PAP	SETLKSEEFQKRLHP	6604	LKSEEFQKR	6644	172
PAP	TVPLSEDQLLYLPFR	6605	LSEDQLLYL	6645	148
PSM	TYSVSFDSLFSAVKN	6606	VSFDSLFSA	6646	627
PSM	VAYINADSSIEGNYT	6607	INADSSIEG	6647	450
PSM	VLRMMNDQLMFLERA	6608	MMNDQLMFL	6648	663
Kallikrein	WGSIEPEEFLRPRSL	6609	IEPEEFLRP	6649	160
PSA	WGSIEPEEFLTPKKL	6610	IEPEEFLTP	6650	156
PSM	WKEFGLDSVELAHYD	6611	FGLDSVELA	6651	103
PAP	YDPLYCESVHNFTLP	6612	LYCESVHNF	6652	213
PSM	YISHNEDGNEIFNT	6613	IINEDGNEI	6653	130
PAP	YRKFLNESYKHEQVY	6614	FLNESYKHE	6654	92

Prostate DR 3b Submotif Peptides

Protein	Sequence	Seq. Id. No.	Core Sequence	Core Seq. Id. No	Position
PSM	AKQIQSQWKEFGLDS	6655	IQSQWKEFG	6675	96
PSM	DALFDIESKVDPSKA	6656	FDIESKVDP	6676	713
PSM	DKIYSISMKHPQEMK	6657	YSISMKHPQ	6677	612
PSM	DMKINCSGKIVIARY	6658	INCSGKIVI	6678	194
PAP	DPLYCESVHNFTLPS	6659	YCESVHNFT	6679	214
PSM	FFKLERDMKINCSGK	6660	LERDMKINC	6680	188
PSM	HVIYAPSSHNKYAGE	6661	YAPSSHNKY	6681	692
PSM	IYNVIGTLRGAVEPD	6662	VIGTLRGAV	6682	358
PAP	KKLIMYSAHDTTVSG	6663	IMYSAHDTT	6683	284
PAP	LTQLGMEQHYELGEY	6664	LGMEQHYEL	6684	73
PSM	MKAFLDELKAENIKK	6665	FLDELKAEN	6685	61
PSM	PSKAWGEVKRQIYVA	6666	AWGEVKRQI	6686	724
PAP	RKFLNESYKHEQVYI	6667	LNESYKHEQ	6687	93
PAP	RSVLAKELKFVTLVF	6668	LAKELKFVT	6688	31
PSM	SIVLPFDCRDYAVVL	6669	LPFDCRDYA	6689	593
PSA	SNDVCAQVHPQKVTK	6670	VCAQVHPQK	6690	179
PSM	TDSAVATARRPRWLC	6671	AVATARRPR	6691	11
PAP	TECMTTNSHQGTEDS	6672	MTTNSHQGT	6692	373
PSM	TEWAEENSRLLQERG	6673	AEENSRLLQ	6693	435
PSM	VHNLTKELKSPDEGF	6674	LTKELKSPD	6694	477

TABLE XXI. Population coverage with combined HLA Supertypes

HLA-SUPERTYPES	PHENOTYPIC FREQUENCY					
	Caucasian	North American Black	Japanese	Chinese	Hispanic	Average
a. Individual Supertypes						
A2	45.8	39.0	42.4	45.9	43.0	43.2
A3	37.5	42.1	45.8	52.7	43.1	44.2
B7	43.2	55.1	57.1	43.0	49.3	49.5
A1	47.1	16.1	21.8	14.7	26.3	25.2
A24	23.9	38.9	58.6	40.1	38.3	40.0
B44	43.0	21.2	42.9	39.1	39.0	37.0
B27	28.4	26.1	13.3	13.9	35.3	23.4
B62	12.6	4.8	36.5	25.4	11.1	18.1
B58	10.0	25.1	1.6	9.0	5.9	10.3
b. Combined Supertypes						
A2, A3, B7	84.3	86.8	89.5	89.8	86.8	87.4
A2, A3, B7, A24, B44, A1	99.5	98.1	100.0	99.5	99.4	99.3
A2, A3, B7, A24, B44, A1, B27, B62, B58	99.9	99.6	100.0	99.8	99.9	99.8

Table XXII. Prostate Antigen Peptides

Antigen Binding affinity ≤ 200nM	Sequence
PSA.117	LMLLRLSEPA
PSA.118	MLLRLSEPAEL
PSA.118	MLLRLSEPA
PSA.143	ALGTTCYA
PSA.161	FLTPKKLQCV
PSA.166	KLQCVDLHV
PAP.6	LLLARAASLSL
PAP.21	LLFFWLDRSV
PAP.30	VLAKELKFV
PAP.92	FLNESYKHEQV
PAP.112	TLMSAMTNL
PAP.135	ILLWQPIPV
PAP.284	IMYSAHDTTV
PAP.299	ALDVYNGLL
PSM.26	LVLAGGFFL
PSM.27	VLAGGFFLL
PSM.168	GMPEGDLVYV
PSM.288	GLPSIPVHPI
PSM.441	LLQERGVAYI
PSM.469	LMYSLVHNL
PSM.662	RMMNDQLMFL
PSM.663	MMNDQLMFL
PSM.667	QLMFLERAFI
PSM.711	ALFDIESKV
HuK2.165	FLRPRSLQCV
HuK2.175	SLHLLSNDMCA

Binding affinity >200nM	Sequence
PSM.4	LLHETDSAV
PSM.25	ALVLAGGFFL
PSM.427	GLLGSTEWA
PSM.514	KLGSGNDFEV

Table XXIIIA A2 supermotif cross-reactive binding data

Peptide	AA	Sequence	Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	A2 Cross-Reactivity
20.0044	9	LLLARAASL	PAP.6	208	13	29	425	--	4
63.0136	11	LLLARAASLSL	PAP.6	8.1	3.1	5.3	80	143	5
60.0201	9	LLLARAASV	PAP.6.V9	18	215	6.7	95	--	4
20.0203	10	LLARAASLSL	PAP.7	500	5.2	63	9250	5714	3
63.0031	10	LLARAASLSV	PAP.7.V10	109	10	21	378	727	4
63.0137	11	AASLSLGFLFL	PAP.11	227	23	53	95	--	4
1419.51	10	SLSLGFLFLL	PAP.13	40	13	403	21	8560	4
1419.52	10	SLSLGFLFLV	PAP.13.V10	1.8	3.9	17	42	355	5
1419.50	9	SLSLGFLFV	PAP.13.V9	77	25	21	93	--	4
60.0203	9	FLFLLFFWV	PAP.18.V9	42	307	625	308	90	4
63.0138	11	FLLFFWLDRSV	PAP.20	14	17	2.8	285	364	5
1097.09	10	LLFFWLDRSV	PAP.21	28	0.60	1.6	231	--	4
1418.23	10	LTFFWLDRSV	PAP.21.T2	118	11	9.6	43	16	5
63.0139	11	LLFFWLDRSVL	PAP.21	65	2.9	2.7	822	4444	3
63.0033	10	SLLAKELKFV	PAP.29.L2	64	5.7	3.8	38	6667	4
1097.171	9	VLAKELKFV	PAP.30	96	3.6	6.7	168	--	4
63.0142	11	VLAKELKFVTL	PAP.30	6.9	8.1	21	25	--	4
63.0034	10	VLAKELKFVV	PAP.30.V10	31	12	189	86	2286	4
1419.55	11	FLNESYKHEQV	PAP.92	29	1.4	5.6	381	6154	4
1177.01	9	TLMSAMTNL	PAP.112	43	0.80	2.9	285	296	5
20.0312	10	TLMSAMTNLA	PAP.112	385	3.6	37	3700	6667	3
63.0037	10	TLMSAMTNLV	PAP.112.V10	63	3.9	12	43	242	5
1419.56	9	TLMSAMTNV	PAP.112.V9	10	2.4	3.6	54	62	5
1419.58	10	LLALFPPEGV	PAP.120.L2	5.0	0.70	1.6	148	163	5
1419.59	10	LVALFPPEGV	PAP.120.V2	156	17	4.8	463	28	5
1419.6	10	ALFPPEGVSI	PAP.122	278	11	133	2643	--	3

-- indicates binding affinity >10,000nM.

Table XXIIIA A2 supermotif cross-reactive binding data

Peptide	AA	Sequence	Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	A2 Cross-Reactivity
1419.61	10	ALFPPEGVSV	PAP.122.V10	15	1.0	18	119	4444	4
63.0041	10	GVSIWNPILV	PAP.128.V10	250	94	23	451	2286	4
60.0207	9	GVSIWNPIV	PAP.128.V9	455	269	909	308	--	3
63.0042	10	PLLLWQPIPV	PAP.134.L2	238	47	19	336	3333	4
1044.04	9	ILLWQPIPV	PAP.135	3.3	39	1.8	71	1702	4
1418.25	9	ITLWQPIPV	PAP.135.T2	34	1720	6.2	26	32	4
1419.69	10	LLWQPIPVHV	PAP.136.V10	25	1.8	17	287	60	5
1166.11	10	GLHGQDLFGI	PAP.196	26	0.90	2.5	315	--	4
1419.62	10	GLHGQDLFGV	PAP.196.V10	12	2.3	3.1	18	--	4
63.0048	10	KLRELSELSV	PAP.234.V10	263	9.1	7.1	49	1818	4
1097.05	10	IMYSAHDTTV	PAP.284	217	1.5	14	411	--	4
1389.06	10	ILYSAHDTTV	PAP.284.L2	385	1.0	15	1480	5714	3
60.0213	9	TVSGLQMAV	PAP.292.V9	294	12	122	195	5.7	5
1177.02	9	ALDVYNGLL	PAP.299	73	29	256	3083	--	3
1419.64	10	LLPPYASCHV	PAP.306.V10	88	15	16	98	5260	4

-- indicates binding affinity >10,000nM.

Table XXIIIB A2 supermotif cross-reactive binding data

Peptide	AA	Sequence	Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	A2 Cross-Reactivity
1126.10	9	VLAGGFFLL	PSM.27	39	0.20	33	31	2857	4
1389.20	9	VLAGGFFLV	PSM.27.V9	26	0.40	5.0	57	216	5
1129.04	10	GMPEGDLVYV	PSM.168	55	3.1	7.1	161	6154	4
1389.22	10	GLPEGDLVYV	PSM.168.L2	42	2.0	2.1	112	964	4
1418.29	10	GTPEGDLVYV	PSM.168.T2	313	134	53	40	571	4
1129.10	10	GLPSIPVHPI	PSM.288	147	2.7	2.1	2467	308	4
1389.24	10	GLPSIPVHPV	PSM.288.V10	55	0.70	0.60	308	121	5
1129.01	10	LLQERGVAYI	PSM.441	179	5.7	6.7	861	--	3
1126.14	9	LMYSLVHNL	PSM.469	64	0.40	2.1	109	320	5
1126.06	10	RMMNDQLMFL	PSM.662	9.8	2.7	7.7	40	--	4
1126.01	9	MMNDQLMFL	PSM.663	11	0.80	1.7	7.6	195	5
1126.16	10	QLMFLERAFI	PSM.667	98	36	91	--	30	4
1129.08	9	ALFDIESKV	PSM.711	85	0.70	1.4	148	8889	4
1418.30	9	ATFDIESKV	PSM.711.T2	238	27	44	82	258	5

-- indicates binding affinity >10,000nM.

Table XXIIIC A2 supermotif cross-reactive binding data

Peptide	AA	Sequence	Source	Alternate Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	A2 Cross-Reactivity
1419.25	11	VVFLTLSVTWI	PSA.1		385	159	63	2846	--	3
63.0185	11	VVFLTLSVTWV	PSA.1.V11		89	88	71	336	--	4
63.0186	11	FLTLSVTWIGV	PSA.3.V11		6.8	3.0	18	65	114	5
60.0216	9	FLTLSVTWV	PSA.3.V9		53	8.4	8.3	49	--	4
60.0217	9	TLSVTWIGV	PSA.5.V9		26	4.9	40	712	229	4
1419.10	11	VLVHPQWVLTA	PSA.49	HuK2.53	294	7.7	101	2056	--	3
1419.11	11	VLVHPQWVLTV	PSA.49.V11	HuK2.53.V11	11	1.5	16	31	8889	4
63.0109	11	DLMLLRLSEPV	PSA.116.V11	HuK2.120.V11	50	57	29	148	2759	4
63.0014	10	LMLLRLSEPA	PSA.117	HuK2.121	200	17	67	925	5000	3
1418.43	10	LMLLRLSEPV	PSA.117.V10	HuK2.121.V10	114	67	29	25	6154	4
1419.02	9	MLLRLSEPA	PSA.118	HuK2.122	195	745	145	49	--	3
1389.10	9	MLLRLSEPV	PSA.118.V9	HuK2.122.V9	36	36	46	638	421	4
1389.12	11	MLLRLSEPAEV	PSA.118.V11		294	331	115	1762	4444	3
1419.01	8	ALGTTCYA	PSA.143	HuK2.147	15	19	13	561	--	3
1389.14	8	ALGTTCYV	PSA.143.V8	HuK2.147.V8	74	6.4	12	264	--	4
1098.02	10	FLTPKKLQCV	PSA.161		52	8.3	13	755	--	3
990.01	9	KLQCVDLHV	PSA.166		79	205	91	6167	--	3
63.0058	10	KLQCVDLHVV	PSA.166.V10		13	84	9.1	500	--	4
60.0220	9	KVTKFMLCV	PSA.187.V9		69	518	53	128	--	3
1419.17	11	PLVCNGVLQGV	PSA.212.V11	HuK2.216.V11	27	127	19	255	4314	4
1418.55	10	LVCNGVLQGV	PSA.213.V10	HuK2.217.V10	10	2.9	12	5.6	3.5	5

-- indicates binding affinity >10,000nM.

Table XXIIID A2 supermotif cross-reactive binding data

Peptide	AA	Sequence	Source	Alternate Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	A2 Cross-Reactivity
1418.13	9	LLLSIALSV	HuK2.4.L2		88	176	147	189	--	4
1418.57	11	ILLSVGCTGAV	HuK2.8.L2		36	33	36	308	--	4
1418.59	11	ITLSVGCTGAV	HuK2.8.T2		294	134	40	206	121	5
1419.05	10	ALSVGCTGAV	HuK2.9		53	75	17	542	--	3
1418.15	9	ALSVGCTGV	HuK2.9.V9		24	17	9.1	264	--	4
1418.35	10	SVGCTGAVPV	HuK2.11.V10		104	287	154	552	216	4
1419.10	11	VLVHPQWVLTA	HuK2.53	PSA.49	294	7.7	101	2056	--	3
1419.11	11	VLVHPQWVLTV	HuK2.53.V11	PSA.49.V11	11	1.6	16	31	9378	4
63.0109	11	DLMLLRLSEPV	HuK2.120.V11	PSA.116.V11	50	57	29	148	2759	4
63.0014	10	LMLLRLSEPA	HuK2.121	PSA.117	200	17	67	925	5000	3
1418.43	10	LMLLRLSEPV	HuK2.121.V10	PSA.117.V10	114	67	29	25	6154	4
1419.02	9	MLLRLSEPA	HuK2.122	PSA.118	195	745	145	49	--	3
1389.10	9	MLLRLSEPV	HuK2.122.V9	PSA.118.V9	36	36	46	638	421	4
1419.01	8	ALGTTCYA	HuK2.147	PSA.143	15	19	13	561	--	3
1389.14	8	ALGTTCYV	HuK2.147.V8	PSA.143.V8	74	6.4	12	264	--	4
1419.07	10	FLRPRSLQCV	HuK2.165		186	4.8	4.2	--	--	3
60.0191	9	SLQCVSLHL	HuK2.170		500	51	417	6167	2581	3
1419.66	10	SLQCVSLHLL	HuK2.170		263	4.9	71	446	5000	4
1418.52	10	SLQCVSLHLV	HuK2.170.V10		13	6.3	2.8	5.2	205	5
1418.19	9	SLQCVSLHV	HuK2.170.V9		56	165	48	4111	1600	3
1419.14	11	SLHLLSNDMCA	HuK2.175		71	4.8	71	--	--	3
1418.66	11	SLHLLSNDMCV	HuK2.175.V11		8.6	0.80	10	2313	2162	3
1419.15	11	HLLSNDMCARA	HuK2.177		417	391	250	374	--	4
1418.67	11	HLLSNDMCARV	HuK2.177.V11		26	1.3	5.3	37	860	4
1418.20	9	HLLSNDMCV	HuK2.177.V9		119	102	278	176	--	4
1418.53	10	LLSNDMCARV	HuK2.178.V10		5.3	0.70	4.3	10	1702	4
1418.71	11	KVTEFMLCAGV	HuK2.191.V11		56	10	26	29	143	5
1418.21	9	KVTEFMLCV	HuK2.191.V9		53	27	31	34	6667	4
1418.22	9	FMLCAGLWV	HuK2.195.V9		29	12	91	51	--	4
1419.17	11	PLVCNGVLQGV	HuK2.216.V11	PSA.212.V11	27	127	19	255	4314	4
1418.55	10	LVCNGVLQGV	HuK2.217.V10	PSA.213.V11	10	2.9	12	5.6	3.5	5

-- indicates binding affinity >10,000nM.

Table XXIVA Immunogenicity of A2 cross-reactive binding peptides and peptide analogs

Peptide ID	AA	Sequence	Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	Cross-Reactivity (≤200nM)	A2 peptide	A2 native	A2 in vivo
1419.51	10	SLSLGFLFLL	PAP.13	40	13	403	21	8560	3			
1419.52	10	SLSLGFLFLV	PAP.13.V10	1.8	3.9	17	42	355	4			
1097.09	10	LLFFWLDRSV	PAP.21	28	0.60	1.6	231	--	3	3/3		0/3
1418.23	10	LTFFWLDRSV	PAP.21.T2	118	11	9.6	43	16	5	3/3	2/3	
1097.17	9	VLAKELKFV	PAP.30	96	3.6	6.7	168	--	4	1/3		0/3
1177.01	9	TLMSAMTNL	PAP.112	43	0.80	2.9	285	296	3	2/2		3/3
1419.58	10	LLALFPPEGV	PAP.120.L2	5.0	0.72	1.6	146	164	5			
1419.61	10	ALFPPEGVSV	PAP.122.V10	15	1.0	18	120	4387	4	1/3	1/3	
1044.04	9	ILLWQPIPV	PAP.135	3.3	39	1.8	71	8511	4	5/5		1/6
1418.25	9	ITLWQPIPV	PAP.135.T2	34	1723	6.2	26	32	4	3/3	2/3	
1419.69	10	LLWQPIPVHV	PAP.136.V10	25	1.8	17	287	60	4			
1166.11	10	GLHGQDLFGI	PAP.196	26	0.9	2.5	315	--	3			
1419.62	10	GLHGQDLFGV	PAP.196.V10	12	2.3	3.2	18	--	4			
1097.05	10	IMYSAHDTTV	PAP.284	217	1.5	14	411	--	2	3/3		0/3
1419.64	10	LLPPYASCHV	PAP.306.V10	88	15	16	98	5260	4			

Table XXIVB Immunogenicity of A2 cross-reactive binding peptide and peptide analogs

Peptide ID	AA	Sequence	Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	Cross-Reactivity (≤200nM)	A2 peptide	A2 native	A2 in vivo
1126.10	9	VLAGGFFLL	PSM.27	39	0.20	33	31	--	4	1/2		3/3
1389.20	9	VLAGGFFLV	PSM.27.V9	26	0.40	5.0	57	216	4	1/2	1/2	
1129.04	10	GMPEGDLVYV	PSM.168	55	3.1	7.1	161	--	4	0/1		1/3
1129.10	10	GLPSIPVHPI	PSM.288	147	2.7	2.1	2467	1538	3	2/4		0/3
1389.24	10	GLPSIPVHPV	PSM.288.V10	55	0.70	0.60	308	121	4	4/4	3/4	
1129.01	10	LLQERGVAYI	PSM.441	179	5.7	6.7	861	--	3	3/3		
1126.14	9	LMYSLVHNL	PSM.469	64	0.40	2.1	109	1600	4	3/3		3/3
1126.06	10	RMMNDQLMFL	PSM.662	9.8	2.7	7.7	40	--	4	1/1		20/22
1126.01	9	MMNDQLMFL	PSM.663	11	0.80	1.7	7.6	976	4	2/2		3/3
1129.08	9	ALFDIESKV	PSM.711	85	0.70	1.4	148	--	4	2/2		3/3

Table XXIVC Immunogenicity of A2 cross-reactive binding peptides and peptide analogs

Peptide ID	AA	Sequence	Source	Alternate Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	Cross-Reactivity (≤200nM)	A2 peptide	A2 native	A2 in vivo
1419.27	11	FLTLSVTWIGV	PSA.3.V11		6.8	3.0	18	65	113	5	3/3	3/3	
1419.11	11	VLVHPQWVLTV	PSA 49.V11	HuK2.53.V11	11	1.6	16	31	9378	4			
1419.13	11	DLMLLRLSEPV	PSA.116.V11	HuK2.120.V11	50	57	29	148	2759	4			
1419.02	9	MLLRLSEPA	PSA.118	HuK2.122	195	745	145	49	--	3			
1389.10	9	MLLRLSEPV	PSA.118.V9	HuK2.122.V9	36	36	46	638	421	3	3/3	1/3	
1419.01	8	ALGTTCYA	PSA.143	PSA.143	15	19	13	562	--	3			
1389.14	8	ALGTTCYV	PSA.143.V8	HuK2.147.V8	74	6.4	12	264	--	3	2/3	1/3	
1098.02	10	FLTPKKLQCV	PSA.161		52	8.3	13	755	--	3	3/4		0/6
990.01	9	KLQCVDLHV	PSA.166		79	205	91	6167	--	2	1/2		1/3
1419.24	10	KLQCVDLHVV	PSA.166.V10		13	84	9.5	502	--	3	1/2	1/2	
1419.17	11	PLVCNGVLQGV	PSA.212.V11	HuK2.216.V11	27	127	19	255	4314	3			

Table XXIVD Immunogenicity of A2 cross-reactive binding peptides and peptide analogs

Peptide	ID	AA	Sequence	Source	Alternate Source	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	Cross-Reactivity (≤200nM)	A2 peptide	A2 native	A2 in vivo
1418.13		9	LLLSIALSV	HuK2.4.L2		88	176	147	189	--	4	2/2	2/2	
1419.05		10	ALSVGCTGAV	HuK2.9		53	75	17	542	--	3			
1419.11		11	VLVHPQWVLTV	HuK2.53.V11	PSA 49.V11	11	1.6	16	31	9378	4	2/2	2/2	
1419.13		11	DLMLLRLSEPV	HuK2.120.V11	PSA.116.V11	50	57	29	148	2759	4	2/2	2/2	
1419.02		9	MLLRLSEPA	HuK2.122	PSA.118	195	745	145	49	--	3			
1389.10		9	MLLRLSEPV	HuK2.122.V9	PSA.118.V9	36	36	46	638	421	3			
1419.01		8	ALGTTCYA	HuK2.147	PSA.143	15	19	13	562	--	3	1/2		
1389.14		8	ALGTTCYV	HuK2.147.V8	PSA.143.V8	74	6.4	12	264	--	3			
1419.07		10	FLRPRSLQCV	HuK2.165		186	4.8	4	--	--	3	1/3		
1419.14		11	SLHLLSNDMCA	HuK2.175		72	4.8	73	--	--	3	1/3		
1419.17		11	PLVCNGVLQGV	HuK2.216.V11	PSA.212.V11	27	127	19	255	4314	3	2/2	2/2	

Table XXV.
DR supermotif and DR3 motif-bearing peptides
cross-reactive binding peptides

Antigen	DR supermotif		DR3
	Motif+	Algorithm+*	Motif+
PAP	67	39/15	21
PSM	45	25/7	4
PSA	108	54/20	31
HuK2	45	21/6	4
Total	265	139/48	60

*Number scoring positive in the combined DR1, DR4w4 and DR7 algorithms (≥1/≥2)